

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:48 ; Search time 20 Seconds
(without alignments)
1723.788 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLLVLL.....ERMGLGCVEDLRSLRQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 2323 | 100.0 | 417 | 2 | US-08-815-469-4 |
| 2 | 2323 | 100.0 | 417 | 2 | US-09-153-927-2 |
| 3 | 2323 | 100.0 | 417 | 2 | US-09-565-918-5 |
| 4 | 2323 | 100.0 | 417 | 2 | US-08-928-069-10 |
| 5 | 2323 | 100.0 | 417 | 2 | US-08-828-683A-6 |
| 6 | 2323 | 100.0 | 417 | 2 | US-09-557-908-4 |
| 7 | 2323 | 100.0 | 417 | 2 | US-09-874-138-5 |
| 8 | 2323 | 100.0 | 417 | 2 | US-09-333-966-4 |
| 9 | 2323 | 100.0 | 417 | 2 | US-09-565-009B-5 |
| 10 | 2323 | 100.0 | 417 | 2 | US-10-175-902-5 |
| 11 | 2323 | 100.0 | 417 | 2 | US-09-314-889-4 |
| 12 | 2323 | 100.0 | 446 | 2 | US-09-949-016-7652 |
| 13 | 2323 | 100.0 | 833 | 2 | US-09-013-895A-5 |
| 14 | 2323 | 100.0 | 833 | 2 | US-09-448-868-5 |
| 15 | 2323 | 100.0 | 833 | 2 | US-10-226-296-5 |
| 16 | 2267 | 97.6 | 428 | 2 | US-08-815-469-2 |
| 17 | 2267 | 97.6 | 428 | 2 | US-09-557-908-2 |
| 18 | 2267 | 97.6 | 428 | 2 | US-09-333-966-2 |
| 19 | 2267 | 97.6 | 428 | 2 | US-09-314-889-2 |
| 20 | 1051 | 45.2 | 181 | 2 | US-08-928-069-1 |
| 21 | 1051 | 45.2 | 181 | 2 | US-08-828-683A-1 |
| 22 | 387.5 | 16.7 | 471 | 2 | US-09-513-007-2 |
| 23 | 387.5 | 16.7 | 471 | 2 | US-09-970-532-2 |
| 24 | 376 | 16.2 | 455 | 1 | US-08-050-319B-25 |
| 25 | 376 | 16.2 | 455 | 1 | US-08-465-982-25 |
| 26 | 376 | 16.2 | 455 | 2 | US-08-406-824A-4 |
| 27 | 374.5 | 16.1 | 909 | 2 | US-09-013-895A-4 |

| | | | | | | |
|----|-------|------|-----|---|------------------|-------------------|
| 28 | 374.5 | 16.1 | 909 | 2 | US-09-448-868-4 | Sequence 4, Appli |
| 29 | 374.5 | 16.1 | 909 | 2 | US-10-226-296-4 | Sequence 4, Appli |
| 30 | 374 | 16.1 | 455 | 1 | US-08-321-668-2 | Sequence 2, Appli |
| 31 | 374 | 16.1 | 455 | 1 | US-08-837-941-2 | Sequence 2, Appli |
| 32 | 374 | 16.1 | 455 | 1 | US-08-126-016-2 | Sequence 2, Appli |
| 33 | 374 | 16.1 | 455 | 2 | US-08-815-469-5 | Sequence 5, Appli |
| 34 | 374 | 16.1 | 455 | 2 | US-09-006-353A-3 | Sequence 5, Appli |
| 35 | 374 | 16.1 | 455 | 2 | US-09-527-236A-5 | Sequence 5, Appli |
| 36 | 374 | 16.1 | 455 | 2 | US-08-054-970-2 | Sequence 4, Appli |
| 37 | 374 | 16.1 | 455 | 2 | US-09-565-918-4 | Sequence 4, Appli |
| 38 | 374 | 16.1 | 455 | 2 | US-09-573-986-3 | Sequence 3, Appli |
| 39 | 374 | 16.1 | 455 | 2 | US-09-027-287-3 | Sequence 3, Appli |
| 40 | 374 | 16.1 | 455 | 2 | US-09-252-656B-3 | Sequence 3, Appli |
| 41 | 374 | 16.1 | 455 | 2 | US-09-523-323-3 | Sequence 3, Appli |
| 42 | 374 | 16.1 | 455 | 2 | US-09-756-854-5 | Sequence 5, Appli |
| 43 | 374 | 16.1 | 455 | 2 | US-09-557-908-5 | Sequence 5, Appli |
| 44 | 374 | 16.1 | 455 | 2 | US-09-874-138-3 | Sequence 3, Appli |
| 45 | 374 | 16.1 | 455 | 2 | US-09-333-966-5 | Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-08-815-469-4
; Sequence 4, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-815-469-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180
DB 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRLQGP 417

RESULT 2

US-09-153-927-2
; Sequence 2, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180

DB 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRLQGP 417

RESULT 3

US-09-565-918-5
; Sequence 5, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180
DB 121 WFVEQVQSCVSSPPFYCQPCDGLHRRHTRLLCSRDDTDCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADDEAG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRLTGLREAE 360
DB 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRLTGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 4

US-08-928-069-10

; Sequence 10, Application US/08928069

; Patent No. 6462176

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; TITLE OF INVENTION: Apo-3 POLYPEPTIDE

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/928,069

; FILING DATE: 11-Sep-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/026943

; FILING DATE: 09/23/1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1052R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 417 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; US-08-928-069-10

; Query Match

; Best Local Similarity 100.0%; Score 2323; DB 2; Length 417;

; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

DB 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120

DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120

QY 121 WFVECVQSVCSVSSPPYCPCLDCGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180

DB 121 WFVECVQSVCSVSSPPYCPCLDCGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180

QY 181 TSTLGSCLPCRCVAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADG 240

DB 181 TSTLGSCLPCRCVAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADG 240

QY 241 MEALTPPPATHLSPLDSAHNTLLAPDSSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300

DB 241 MEALTPPPATHLSPLDSAHNTLLAPDSSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRLTGLREAE 360
DB 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRLTGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 5

US-08-828-683A-6

; Sequence 6, Application US/08828683A

; Patent No. 6469144

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A

; FILING DATE: 31-Mar-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/625328

; FILING DATE: 1-Apr-1996

; APPLICATION NUMBER: 08/710802

; FILING DATE: 23-Sep-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 417 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

; US-08-828-683A-6

; Query Match

; Best Local Similarity 100.0%; Score 2323; DB 2; Length 417;

; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

DB 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120

DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120

QY 121 WFVECVQSVCSVSSPPYCPCLDCGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180

DB 121 WFVECVQSVCSVSSPPYCPCLDCGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180

QY 181 TSTLGSCLPCRCVAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADG 240

DB 181 TSTLGSCLPCRCVAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADG 240

QY 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
DB 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
QY 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 6
US-09-557-908-4
; Sequence 4, Application US/09557908
; Patent No. 6713061
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; FILE REFERENCE: 1488.0310008
; CURRENT APPLICATION NUMBER: US/09/557,908
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-908-4
Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCCCKPG 120
QY 121 WFVECVQSVCSVPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
DB 121 WFVECVQSVCSVPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTRHCWPHKPLVTADEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTRHCWPHKPLVTADEAG 240
QY 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
DB 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
QY 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417

DB 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417
RESULT 7
US-09-874-138-5
; Sequence 5, Application US/09874138
; Patent No. 6743625
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-5
Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCCCKPG 120
QY 121 WFVECVQSVCSVPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
DB 121 WFVECVQSVCSVPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTRHCWPHKPLVTADEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTRHCWPHKPLVTADEAG 240
QY 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
DB 241 MEALTPPPATHSLDLSAHTLLAPPDSSSEKICTVQLVGNWSWTPGYPTQALCPQVTSW 300
QY 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRAGPAAAPTLLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGVAAALERMGLDGCVEDLRSRLQRP 417

Db 361 IEAVEIGRFRDQQYEMLKRWQQQAGVAVYAAERMGDGCVEDLRSRLQRP 417

RESULT 8

US-09-333-966-4
; Sequence 4, Application US/09333966
; Patent No. 6759513
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. 6759513 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-333-966-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSSPFYCQPCDCLCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
Db 121 WFVEQVQSCVSSSPFYCQPCDCLCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180

QY 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHPHKPLVLTADAG 240
Db 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHPHKPLVLTADAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKI CTVQLVGNSTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKI CTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDNDVNDVAPARWKEFVRTLGUREAE 360
Db 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDNDVNDVAPARWKEFVRTLGUREAE 360
QY 361 IEAVEIGRFRDQQYEMLKRWQQQAGVAVYAAERMGDGCVEDLRSRLQRP 417
Db 361 IEAVEIGRFRDQQYEMLKRWQQQAGVAVYAAERMGDGCVEDLRSRLQRP 417

RESULT 9

US-09-565-009B-5
; Sequence 5, Application US/09565009B
; Patent No. 6872568
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/565,009B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-565-009B-5

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSSPFYCQPCDCLCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
Db 121 WFVEQVQSCVSSSPFYCQPCDCLCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
QY 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHPHKPLVLTADAG 240
Db 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYYRHCHPHKPLVLTADAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKI CTVQLVGNSTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKI CTVQLVGNSTPGYPETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQOQAGLGAUYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQOQAGLGAUYAALERMGLDGCVEDLRSRLQRP 417
RESULT 10
US-10-175-902-5
; Sequence 5, Application US/10175902
; Patent No. 6902910
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/10/175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5
Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
Db 121 WFVEQVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
QY 181 TSTLGSCTPCERCAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
Db 181 TSTLGSCTPCERCAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
QY 241 MEALTPPAPTHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
Db 241 MEALTPPAPTHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQOQAGLGAUYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQOQAGLGAUYAALERMGLDGCVEDLRSRLQRP 417

RESULT 11
US-09-314-889-4
; Sequence 4, Application US/09314889
; Patent No. 6951735
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,469
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-314-889-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
Db 121 WFVEQVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
QY 181 TSTLGSCTPCERCAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
Db 181 TSTLGSCTPCERCAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240

| | | | |
|----|-----|--|-----|
| Qy | 241 | MEALTPPPATHSLPDSAHTLLAPPDSSSEKICTVOLVGNSTWTPGYPETQEALCPQVTSW | 300 |
| Db | 241 | MEALTPPPATHSLPDSAHTLLAPPDSSSEKICTVOLVGNSTWTPGYPETQEALCPQVTSW | 300 |
| Qy | 301 | DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| Db | 301 | DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| Qy | 361 | IEAVEVEIGRFRDQOYEMLKWRQOOPAGLGAIVYAALERMGLDGCVEDLRSRLQRP | 417 |
| Db | 361 | IEAVEVEIGRFRDQOYEMLKWRQOOPAGLGAIVYAALERMGLDGCVEDLRSRLQRP | 417 |

RESULT 12

```

US-09-949-016-7652
; Sequence 7652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7652
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7652

```

```
Query Match      100.0%; Score 2323; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. NO. 3.8e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

| | | | |
|----|-----|---|-----|
| Qy | 1 | MEQPRGCAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGPCAGHYLKAP | 60 |
| Db | 30 | MEQPRGCAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGPCAGHYLKAP | 89 |
| Qy | 61 | CTEPCGNSTCLVCPQDTPFLAWENHNSECRCQACDEQASOVALLENCASAVADTRCGCKPG | 120 |
| Db | 90 | CTEPCGNSTCLVCPQDTPFLAWENHNSECRCQACDEQASOVALLENCASAVADTRCGCKPG | 149 |
| Qy | 121 | WFVECVQSVQSVSSPFYCPCLDCGALHRRHLLCSRRDTCGTCPLPGFYEHGDCVSCP | 180 |
| Db | 150 | WFVECVQSVQSVSSPFYCPCLDCGALHRRHLLCSRRDTCGTCPLPGFYEHGDCVSCP | 209 |
| Qy | 181 | TSTLGSCPERRCAAVCGWRQFWVQVLLAGLVPLLLGATLVTYTRHCWPHPLVTADBAE | 240 |
| Db | 210 | TSTLGSCPERRCAAVCGWRQFWVQVLLAGLVPLLLGATLVTYTRHCWPHPLVTADBAE | 269 |
| Qy | 241 | MEALTTPPPATHLSPLDSAHNTLLAPDSEKICTVQLVGNSTWPGVPETQEALCPQVTSW | 300 |
| Db | 270 | MEALTTPPPATHLSPLDSAHNTLLAPDSEKICTVQLVGNSTWPGVPETQEALCPQVTSW | 329 |
| Qy | 301 | DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLREAE | 360 |
| Db | 330 | DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLREAE | 389 |
| Qy | 361 | IEAVEVEIGRFRDQOQYEMLEKWRQOQAPAGLGAVYAALERMGLDGCVEDLRSRLQRGP | 417 |
| Db | 390 | IEAVEVEIGRFRDQOQYEMLEKWRQOQAPAGLGAVYAALERMGLDGCVEDLRSRLQRGP | 446 |

RESULT 13

US-09-013-895A-5
; Sequence 5, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

| Query Match | 100.0.0%; Score 2323; DB 2; Length 833; |
|--|---|
| Best Local Similarity | 100.0.0%; Pred. No. 8.4e-193; |
| Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY 1 | MEQPRGCAVAALLLVLGARAQGGTSPRCDACGDFHKKI GLFCRCRCPAGHYLKAP 60 |
| DB | |
| QY 1 | MEQPRGCAVAALLLVLGARAQGGTSPRCDACGDFHKKI GLFCRCRCPAGHYLKAP 60 |
| DB | |
| QY 61 | CTPFCNGSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSAVADTRCGCKPG 120 |
| DB | |
| QY 61 | CTPFCNGSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSAVADTRCGCKPG 120 |
| DB | |
| QY 121 | WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTCLPGFYEHGDCGVSCP 180 |
| DB | |
| QY 121 | WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTCLPGFYEHGDCGVSCP 180 |
| DB | |
| QY 181 | TSTLGSPCRCAAVCGWRQFWQVLLAGLWPLLIGATLTYTYRHCWPHKPIVLTAD EAG 240 |
| DB | |
| QY 181 | TSTLGSPCRCAAVCGWRQFWQVLLAGLWPLLIGATLTYTYRHCWPHKPIVLTAD EAG 240 |
| DB | |
| QY 241 | MEALTPTTPATHLSPLD SAHTLLAPPDSSEKICTVQLVGNENSWTPGYETQALCPQVTSW 300 |
| DB | |
| QY 241 | MEALTPTTPATHLSPLD SAHTLLAPPDSSEKICTVQLVGNENSWTPGYETQALCPQVTSW 300 |
| DB | |
| QY 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGREAE 360 |
| DB | |
| QY 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGREAE 360 |
| DB | |

QY 361 IEAVEVEIGRFRDQOYEMLKRWQOOPAGLGAIVAAALERMGLDGCVEDLRSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWQOOPAGLGAIVAAALERMGLDGCVEDLRSRLQGRP 417

RESULT 14

US-09-448-868-5
; Sequence 5, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-448-868-5

Query Match 100.0%; Score 2323; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 8,4e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLLVILGARAQGGTRSPRCDGDFHKKITGLFCCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLLVILGARAQGGTRSPRCDGDFHKKITGLFCCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTPECGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSVSSPFYQPCPLDCGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSVSSPFYQPCPLDCGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADEAG 240

Db 181 TSTLGSPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADEAG 240
QY 241 MEALTTPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
Db 241 MEALTTPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
QY 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPQLYDVMDAVPARRWKSEFVRTILGLEAE 360
Db 301 DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPQLYDVMDAVPARRWKSEFVRTILGLEAE 360
QY 361 IEAVEVEIGRFRDQOYEMLKRWQOOPAGLGAIVAAALERMGLDGCVEDLRSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWQOOPAGLGAIVAAALERMGLDGCVEDLRSRLQGRP 417

RESULT 15

US-10-226-296-5
; Sequence 5, Application US/10226296
; Patent No. 6943020
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-AUG-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-226-296-5

Query Match 100.0%; Score 2323; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 8,4e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLLVILGARAQGGTRSPRCDGDFHKKITGLFCCRCGCPAGHYLKAP 60

| | | | |
|----|-----|---|-----|
| Db | 1 | MEQRPRGCAVAAALLLVILGARAAQGGTRSPRCDGAGDFHKKIKIGLFCCRGCPCAGHYLKAP | 60 |
| Qy | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| Qy | 121 | WFVEQVSOQVSSPFYCPCLDCGALHRRHRLLCSSRRDTCGTCLPGFYEHGDCVSCP | 180 |
| Db | 121 | WFVEQVSOQVSSPFYCPCLDCGALHRRHRLLCSSRRDTCGTCLPGFYEHGDCVSCP | 180 |
| Qy | 181 | TSTLGSCEPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWPHKPLVTADAG | 240 |
| Db | 181 | TSTLGSCEPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWPHKPLVTADAG | 240 |
| Qy | 241 | MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSTPGYPETOALCPQVTWSW | 300 |
| Db | 241 | MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSTPGYPETOALCPQVTWSW | 300 |
| Qy | 301 | DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| Db | 301 | DQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| Qy | 361 | IEAVEVEIGFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP | 417 |
| Db | 361 | IEAVEVEIGFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP | 417 |

Search completed: March 20, 2006, 08:00:16
Job time : 21 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:25 ; Search time 27 Seconds
(without alignments)
1486.014 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAAAALLLVLL.....ERMGLDGVEDLRSRLQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 415 | 17.9 | 461 | JC4302 | tumor necrosis fac |
| 2 | 404.5 | 17.4 | 454 | GQWST1 | tumor necrosis fac |
| 3 | 394.5 | 17.0 | 461 | GQRTT1 | tumor necrosis fac |
| 4 | 374 | 16.1 | 455 | GQRTU1 | tumor necrosis fac |
| 5 | 199.5 | 8.6 | 335 | A40036 | apoptosis-mediatin |
| 6 | 196 | 8.4 | 327 | A46484 | apoptosis-mediatin |
| 7 | 175 | 7.5 | 324 | JC2395 | Fas antigen precur |
| 8 | 168 | 7.2 | 314 | I37383 | FAS soluble protei |
| 9 | 166 | 7.1 | 435 | I54182 | tumor necrosis fac |
| 10 | 163.5 | 7.0 | 1548 | S34583 | serine proteinase |
| 11 | 162.5 | 7.0 | 349 | D36858 | gene GAR protein - |
| 12 | 159.5 | 6.9 | 348 | T28623 | hypothetical prote |
| 13 | 158 | 6.8 | 425 | A26431 | nerve growth facto |
| 14 | 158 | 6.8 | 1574 | T13954 | MEGF6 protein - ra |
| 15 | 155.5 | 6.7 | 427 | GQHUN | nerve growth facto |
| 16 | 154.5 | 6.7 | 349 | D72175 | G2R protein - vari |
| 17 | 153.5 | 6.6 | 272 | I48700 | gene ox40 protein |
| 18 | 153.5 | 6.6 | 651 | JC7705 | death receptor-6 - |
| 19 | 153.5 | 6.6 | 915 | A48225 | subtilisin-like pr |
| 20 | 149.5 | 6.4 | 3707 | S18252 | heparan sulfate pr |
| 21 | 148 | 6.4 | 2823 | F87908 | protein T2A3.8 [i |
| 22 | 148 | 6.4 | 2823 | T23064 | hypothetical prote |
| 23 | 148 | 6.4 | 3102 | T43291 | laminin alpha chai |
| 24 | 147.5 | 6.3 | 1801 | 1MMRTS | laminin beta-2 cha |
| 25 | 146.5 | 6.3 | 2531 | T31070 | notch homolog - se |
| 26 | 146 | 6.3 | 277 | A60771 | B-cell activation |
| 27 | 146 | 6.3 | 667 | A48579 | trophozoite surfac |
| 28 | 145.5 | 6.3 | 416 | 1JN006 | nerve growth facto |
| 29 | 145 | 6.2 | 3635 | T10053 | laminin alpha 5 ch |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 30 | 144.5 | 6.2 | 326 | 1 | GQVZML | T2 protein - myxom |
| 31 | 144.5 | 6.2 | 1680 | 2 | A43434 | furin (EC 3.4.21.7 |
| 32 | 143.5 | 6.2 | 915 | 2 | B48225 | probable proprotel |
| 33 | 143.5 | 6.2 | 4391 | 2 | A38096 | perlecan precursor |
| 34 | 142 | 6.1 | 1557 | 2 | T28811 | hypothetical prote |
| 35 | 141.5 | 6.1 | 686 | 2 | JC7569 | Delta-4 protein - |
| 36 | 138.5 | 6.0 | 1299 | 2 | T43251 | furin (EC 3.4.21.7 |
| 37 | 138 | 5.9 | 271 | 2 | S12783 | OX40 antigen precu |
| 38 | 138 | 5.9 | 305 | 2 | A46476 | B cell-associated |
| 39 | 138 | 5.9 | 1607 | 1 | MMMSB2 | laminin gamma-1 ch |
| 40 | 138 | 5.9 | 1609 | 1 | MMHUB2 | laminin gamma-1 ch |
| 41 | 137.5 | 5.9 | 642 | 1 | S52111 | uromodulin precurs |
| 42 | 137.5 | 5.9 | 1798 | 2 | S53869 | laminin beta-2 cha |
| 43 | 136.5 | 5.9 | 260 | 1 | A46517 | CD27 antigen precu |
| 44 | 136.5 | 5.9 | 2219 | 2 | T27684 | hypothetical prote |
| 45 | 136.5 | 5.9 | 3712 | 2 | S18253 | laminin alpha-1 ch |

ALIGNMENTS

RESULT 1

JC4302

tumor necrosis factor receptor p55 precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: JC4302; PC4093

R:Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A:Reference number: JC4302; MUID:96011645; PMID:7590278

A:Accession: JC4302

A:Molecule type: mRNA

A:Residues: 1-461 <SUT>

A:Cross-references: UNIPROT:P50555; UNIPARC:UPI00001372A9; GB:U19994; NID:g1141752; PIDN

A:Accession: PC4093

A:Molecule type: protein

A:Residues: 1-7 <SU2>

A:Cross-references: UNIPARC:UPI0000176767

A:Experimental source: kidney cell line 15

A:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <WAT>

F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NGF>

F:211-231/Domain: transmembrane #status predicted <TMW>

F:361-447/Domain: signal transduction #status predicted <SIT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.9%; Score 415; DB 2; Length 461;

Best Local Similarity 30.5%; Pred. No. 8.7e-21;

Matches 140; Conservative 44; Mismatches 201; Indels 74; Gaps 18;

| | | | |
|----|-----|--|--|
| QY | 11 | VAAALLVLLGARAQ-----GTRSPR-----CDCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62 | |
| DB | 14 | VLRALLVDVYPAGVHGLVLPDGRKRESLCPQGKYSHPNRSICCTCKHGYLLNDCL 73 | |
| QY | 63 | BFCGNSTCLVCPQDFTFLAWENHNHSEFCARCAQDEQASQVALENCASAVADTRCGCKPGWF 122 | |
| DB | 74 | GFGLDTRDCRCNGIFTASEN-HLTQCLSCSKRSEMSQVEISPTVDRDTVCGCRKN-- 130 | |
| QY | 123 | VSCQSVQCVSSPFFVCPQCLDCGALHRRHLRLC-SRRDTCGTCLPGFVEHGGGCVSCPT 191 | |
| DB | 131 | ---QYRKYWSSETLFOCLNGLCP--NGTVQLPCLERQDTIC-NCHSGFFLRKDEKVCVCVN 184 | |
| QY | 182 | STLGSCPERCAVCGWRQMF-----WVQVLLAGLVVPLLIIGATLTITYRHCPH--- 230 | |
| DB | 185 | CKNADCKNLCPATSETRNDQDTGTVTLLPLVIFFLGLCLAFLLVGLACKYQKWKPLYS 244 | |

QY 231 -----KPLVTADEAGMEALTPPPATHLSPLD--SAHTLLAPDSEKICTV 274
Db 245 IICGKSTPVKEGPEPLATAPSG-----PITTFSPISPSPTTTFSPVPSPISSP 297
QY 275 QLVGNSWT---PGVPETQALCPQVWWSWDLPSRLGPAAPLTPS-----RSPAG 323
Db 298 TFTPQWSNICKVTSPPKEIAPPQAG-----PILPMPASTVPTPLPKWGGSAHSAHS 352
QY 324 SPAMQLQGP-QLYDVMDVAPARWKEFVFTLGLREAEIEAVEVEIGR-FRDOQYEMLKR 381
Db 353 APLQADADPATLYAVVDGVPPTKWEFVRRLGSEHEIERLELQNGRCUREAQYSLAE 412
QY 382 WRQ---QQPAGLAVYAALERMGLDGCVEDLRSLRQGP 417
Db 413 WRRTSREATLELGSVLDMDLGCLDEIEAL-RGP 450
RESULT 2
QMSST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
A;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID: 91187885; PMID: 1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: UNIPROT: P25118; UNIPARC: UPI000002348D; GB: M60468; NID: g199825; PID:
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID: 91246168; PMID: 1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: UNIPARC: UPI000002348D; GB: M60468; NID: g199825; PID: AAA39751.1; PID:
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenberghis, A.M.; Gray, P.W.; Feidma
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A;Reference number: S16677; MUID: 91285014; PMID: 1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: UNIPARC: UPI000002348D; EMBL: X59238; NID: g53578; PID: CAA41922.1; PID:
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID: 92039815; PMID: 1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: UNIPARC: UPI000002348D; EMBL: X57796; NID: g54848; PID: CAA40936.1; PID:
R;Babo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell
A;Reference number: I54532; MUID: 94245292; PMID: 8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: UNIPARC: UPI000002348D; GB: I26349; NID: g430732; PID: AAAS9361.1; PID:
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: I57826; MUID: 93156721; PMID: 8381516
A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393, 'G', 395-454 <RE2>

A;Cross-references: UNIPARC: UPI0000161D7C; GB: M76656; NID: g202100; PID: AAA40465.1; PID:
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) #status predicted
Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 4.4e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;
QY 11 VAAALLLVILGARAQGGT-----RSPRCDCAGDFHKIGLFCRCGCPAGHYLKA 59
Db 11 LSLVLLALLMGHPSGVGTGLVPSLGLDREKRDLSLCPQKQKVHSHKNSICTCTKCHKGTLYVS 70
QY 60 PCTPCGNSLTCVCPQDTFLAVENHNSCARCQACQEQASQVALENCSAVADTRCGCKP 119
Db 71 DCPSGRDVTVCRCERKGTFTASQNYLR-QCLSKCTCKEMSQVEISPCQADKDTVCCK- 128
QY 120 GWFEVQCVQCVSSSPFYQPCPLDCCALHRHRLTLLCRRDTCGTCPLPYEYHGDGCVSC 179
Db 129 -----ENQFQYLSETHFCQVDCSPC--FNGTVTIPCKETQNTVCNCHAGFLRESECVPC 182
QY 180 PYSGLGSCP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLGLATLYTY 224
Db 183 -----SHCKKNECMKLCPLPPPLAVNTVPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY 237
QY 225 RHQWP-----HKPLVTADEAGMEALTPPPATHLSPLDLSAHTLL-----APPSSEK 270
Db 238 PRWRPEVYIIICRDPVVKKEKAGKELTAPSPAFSTGPNLTGFSPTGFSPPVSSSTP 297
QY 271 ICTVQLVGNWSW-----TPGY-PETQALC----PQVTSWDLPSRLGPAAP 314
Db 298 ISPI-FGPNWHFMPVSEVVPVTPQADPLLYESLCSVPAPTSVQKWED----- 344
QY 315 TISPEPAGSPAMQLQPGPOLVDMDVAPARWKEFVFTLGLREAEIEAVEVEIGR-FRD 373
Db 345 SAHPQRPDNLAL-----LYAVDGVPPARWKEFMRFMGLSEHERLEMQNGRCLRE 398
QY 374 QQYEMLKRWRQOQPA---GLGAVYAALERMGLDGCVEDLRSLRQGP 417
Db 399 AQYSMLDEAWRRTPRHEDTLEVVGLVLSKNNLACLENLEAL-RNP 444
RESULT 3
QQRRT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: B36555
R;Himpler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A;Reference number: A36555; MUID: 91090841; PMID: 1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HM>
A;Cross-references: UNIPROT: P22934; UNIPARC: UPI00001372AA; GB: M63122; NID: g207361; PID:
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein

A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Cross-references: UNIPARC:UPI00001736E2
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Cross-references: UNIPARC:UPI00001736E3
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biochim. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Cross-references: UNIPARC:UPI00001736E4
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Domain: product; tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (Asn) #status predicted

Query Match 16.1%; Score 374; DB 1; Length 455;
Best Local Similarity 28.3%; Pred. No. 5e-18;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;

QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKIIGLFCRCGCPAGHYLKAPCTE 63
DB 15 LLELLGVYPSGVIGLVPHLGDRKRDVCPQGYIHPQNNISCTCKCHKGTLYLNDGPG 74
QY 64 PCGNSTCLVCPQDTFLAWENHNHSECAQCDQASQVALENCASAVADTRCCGKPGWFV 123
DB 75 PQQDTDCRECSGFTASENHLR-HCLSCSKCKRMGQVEISSCTVDRTVCGCRKNQYR 133
QY 124 EC---QVSQCVSSPPFCQCLDGCALHRRHRLLCRRDTCGTLPGFYEHGDCGVSCP 180
DB 134 HYSENILFQC-----FNCISCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENEVCSC- 182
QY 181 TSTLGSCEP---RCAAVC-----GWQFMFWQVLLAGLVPLLLGATLTYTRH 226
DB 183 ----SNCKKSLETKLCPQIENVKGTEDSGTTLVPLVIFGLCLLSLLFGLMYRYQR 238
QY 227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS-----AHTLLAPDSSEKIC 272
DB 239 -WKSCLYSIVCGKSTPEKELEGSTTKP---LAPNPSFSPTGFTPTLGFSPVPSSTFT 294
QY 273 TVQLVGNWTPGYPETQALCPQVWTSWDLPSRALGSP-----AAAPTLSL- 318
DB 295 S-----SSTYTPGD-----CPNFA-----APREVAAPPQGDPIATALASDPIPNFL 338
QY 319 ---ESPAGSPAMMLQPGP-QLYDMDAVPARRWKEFVITGLREARIEAVEVEIGR-FRD 373
DB 339 QKWEDSAHKQSLDTPDDPATLYAVENVPLRWKEFVRRGLGLSDHEIDRLQLNGRCLE 398

QY 374 QQYEMLKRRWQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
DB 399 AQYSLMATWRRRTPRREATLELGLRVLRDMDLGLGLEDIEAL 441

RESULT 5

A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004
C:Accession: A40036; S24543; J38142
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate
A:Reference number: A40036; MUID:91309137; PMID:1713127
A:Accession: A40036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <ITO>
A:Cross-references: UNIPROT:P25445; UNIPARC:UPI000003060C; GB:M67454; NID:g182409; PIDN:J
R:Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A:Reference number: S24543
A:Accession: S24543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <KRA>
A:Cross-references: UNIPARC:UPI000003060C; EMBL:X63717; NID:g28741; PID:g28742
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richter, J. Biol. Chem. 267, 10709-10715, 1992
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member of
A:Reference number: A38142; MUID:92268122; PMID:1375228
A:Accession: A38142
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-134, 'Q', 136-335 <OEH>
A:Cross-references: UNIPARC:UPI000014E7A3
A:Experimental source: SKW6.4 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)
A:Note: in NCBI backbone the source is designated as mouse
C:Genetics:
A:Gene: GDB:APT1
A:Cross-references: GDB:132671; OMIM:134637
A:Map position: 10q24.1-10q24.1
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C:Keywords: apoptosis; surface antigen; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:85-128/Domain: NGF receptor repeat homology <NG4>
F:174-190/Domain: transmembrane #status predicted <TMM>

Query Match 8.6%; Score 199.5; DB 2; Length 335;
Best Local Similarity 21.4%; Pred. No. 2.2e-06;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLPCCGCGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECAQCDQASQVA 103
DB 56 GQCHPCPCGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKCRRCRLCDEGHGLEV 115
QY 104 LENCASAVADTRCCGKPGWFVEQCQVSCVSSPPFCQCLDGCALHRRHRLLCRRDTCG 163
DB 116 EINCTRTQNTCKCKNFP-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYEHGDCVSCPTSTLGSCEPCERCAAVCGWR-OMFWQVLLAGLVPLLLGATLTY 222
DB 150 -----EHGI-IKECTLTSTNTCKEE-----GSRNLGWLCLL--LPIPLIVWVRKE 194
QY 223 TYRHCHWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTL---LAPDSSEKI CTIVQLVGN 279
DB 195 VQKTCRKH-----KENQG-----SHESPTLNPTETVAINLSDVLSKYITTI----- 236
QY 280 SWTPGYPETQALCPQVWTSWDLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVM 339

```
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: UNIPROT:Q63199; UNIPARC:UPI00001370ED; DDBJ:D26112; NID:9468486; PID:
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62, 'RFT', <K12>
A;Cross-references: UNIPARC:UPI000011F885; DDBJ:D26113; NID:9468488; PIDN:BAA05109.1; PI1
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-79/Domain: Fas antigen #status predicted <NAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TM>

Query Match 7.5%; Score 175; DB 2; Length 324;
Best Local Similarity 28.5%; Pred. No. 9.6e-05;
Matches 43; Conservative 17; Mismatches 67; Indels 24; Gaps 5;

QY 11 VAAALLVLGG---ARAQG-----GTRSPRCDCAGDFHKIGLFCRCGCPAG 54
DB 4 IMAVLPLVLGAPLNVRMGTDSIFGELKRSVRTDNNCSGLY-QVGFPCQCPQG 62

QY 55 HYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQASQVALENSAVADTR 114
DB 63 ERKVKDCTTSGGAPTCPTCEGSEYTDKHSYDKRCARCAFCDEGHGLEVEINCTRIQNTK 122

QY 115 CGCKPQWFVECVQSVSSPPFYCQPCLDG 145
DB 123 CRCKENFY--CNASLC-----DHCYHCTSCG 146

RESULT 8
I37383
FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I37383
R;Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A;Reference number: I37383; MUID:95181785; PMID:7533181
A;Accession: I37383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: UNIPROT:P25445; UNIPARC:UPI000002B592; EMBL:Z47993; NID:9728578; PID:
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

Query Match 7.2%; Score 168; DB 2; Length 314;
Best Local Similarity 19.1%; Pred. No. 0.00028;
Matches 66; Conservative 37; Mismatches 100; Indels 142; Gaps 10;

QY 44 GLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQASQVA 103
DB 56 GQFCHKPCPPGERKARDCTVNGDEPCVQCEGKEYTDKAHFSKCRCLCDDEGHGLEV 115

QY 104 LENCASAVADTRCGCKPQWFVECVQSVSSPPFYCQPCLDGALHRRHRLLCRRRDTDCG 163
DB 116 EINCTRTQNTKCRCKENFY-----CNSTVCSHCDDPCTKC----- 149

QY 164 TCLPGFYHGDGCVSCPTSTLGSCEPCARCAVCQWRQFWQVLLAGLVVPLLLGATLTYT 223
DB 150 -----EHGI-IKECTLTSTNTCKSE-----VKRKEV 174

apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins,
J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas ant
A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Accession: A46484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <NAT>
A;Cross-references: UNIPROT:P25446; UNIPARC:UPI0000027457; GB:M83649; NID:9193225; PIDN:
A;Experimental source: B6M3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable element
A;Reference number: A47254; MUID:93189576; PMID:7680478
A;Accession: A47254
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
A;Cross-references: UNIPARC:UPI0000170C50; GB:S56490; NID:9298505; PIDN:AAB25700.1; PID:
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 8.4%; Score 196; DB 2; Length 327;
Best Local Similarity 23.8%; Pred. No. 3.7e-06;
Matches 62; Conservative 25; Mismatches 109; Indels 64; Gaps 8;

QY 13 AALLLVLLGARAQGGTSPRC-----DCAGDFHKIGLFCRCGCPAGHY 56
DB 6 AVLPLVLGASQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQG-GPCCQCPQPKK 64

QY 57 LKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDQASQVALENSAVADTRCG 116
DB 65 KVEDCKWNGTPTCAPCTEKGKYMDKHYADKRCRCLCDEHGLEVEINCTLTQNTKCK 124

QY 117 CKPGWFVECVQSVSSPPFYCQPCLDGALHRRHRLLCRRRDTDCGTCPLPGFYHGDGC 176
DB 125 CKP-----DFYCDSE-----PG-CEHCVRG 142

QY 177 VSCPTSTLGSCEPCARCAVC---GWRQFWQVLLAGLVVPLLLGATLTYTYRHCWPKPL 233
DB 143 ASCEHGTLEPTCTATSNCRKQSPNRLWLLTLV-LLIPLVF-IVRYKRRKRCWRRQD 200

QY 234 VTADAGMEALTPPPATHLS 253
DB 201 DPESRTSSRETIPMNASNLS 220

RESULT 7
JC2395
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
```


MEGF6 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13954
R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 54, 27-34, 1998
A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A/Reference number: Z14126; MUID:98360089; PMID:9693030
A/Accession: T13954
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1574 <NAK>
A/Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293;
A/Experimental source: strain Sprague-Dawley; brain
C/Genetics:
A/Gene: MEGF6

Query Match 6.8%; Score 158; DB 2; Length 1574;
Best Local Similarity 24.5%; Pred. No. 0.0061;
Matches 90; Conservative 16; Mismatches 120; Indels 142; Gaps 23;

QY 30 SPCDCAGDHHKIGLFCRCGPAGHY-----LKAQCTEPCGNSTCLV----- 72
Db 933 SGACTCPAGWR---GSFCEHACGAGFGLDCLDSACNCSGAPCDVATGSCICPAGRWGPR 989

QY 73 ----CPQDTFLAWENHNHNSCARCOACDEQASOQVALENCASAVADTRCGCKPGWF----- 122
Db 990 CAQSCPLTF-----GLNCSQICTCFNGAS-----CDSVTG-QCHCAPGWMGPCLQ 1035

QY 123 -----VSCQVSSQVSSPFFCQCL-DGALHRRHLLCRRDTCCTCLPGFVY-- 171
Db 1036 ACPPGLYKNCQHS-CLCRNGRCDPTLGQCTCEGWTGLACENE-----CLPGHYAAG 1088

QY 172 -----HGDGC-----VSCPTSLTG-SCPERCA-----AVC----- 195
Db 1089 COLNCSCLHGGICDRLTGHCLCPAGWTGDKQSCSVSGTFFGVHCEHCACRKGASCHVT 1148

QY 196 -----GWQMFVQVLLAGLVVLLLGATLTVTYRHCHWPHKPLVTADAGMEALTPPP 248
Db 1149 GACFCPPGWRGPHCEQACPRGWEACACRCLCPFNASC--HH--VTG-----ECRCPPG 1199

QY 249 ATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPG-YPETQAL--CPQVTVSWDQLPS 305
Db 1200 FTGL-----SCEQAC-----QPGTFGKDCHELCQCPGETWACD--PA 1234

QY 306 RALGPAAA 313
Db 1235 SGVCTCAA 1242

RESULT 15
QHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N/Alternate names: NGF receptor
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C/Accession: A25218; A60204; S21689; I57638
R/Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A/Title: Expression and structure of the human NGF receptor.
A/Reference number: A25218; MUID:87051725; PMID:3022937
A/Accession: A25218
A/Molecule type: mRNA
A/Residues: 1-427 <JOH>
A/Cross-references: UNIPROT:P08138; UNIPARC:UPI0000049854; GB:M14764; NID:g189204; PIDN:
R/Warano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A/Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A/Reference number: A60204; MUID:87085574; PMID:3025363
A/Accession: A60204
A/Molecule type: protein
A/Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>
A/Cross-references: UNIPARC:UPI000001736DA

A/Experimental source: melanoma cell line A875
A/Note: this sequence has been corrected by a note added in proof to follow the nucleotide
R/Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A/Title: Structural domains of the extracellular domain of human nerve growth factor rec
A/Reference number: S21689; MUID:92198017; PMID:1372492
A/Accession: S21689
A/Status: preliminary
A/Molecule type: protein
A/Residues: 183-208 <VIS>
A/Cross-references: UNIPARC:UPI000001736DB
R/Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A/Title: A constitutive promoter directs expression of the nerve growth factor receptor
A/Reference number: I57638; MUID:89096903; PMID:2850481
A/Accession: I57638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-22 <RES>
A/Cross-references: UNIPARC:UPI000016ADDE; GB:M21621; NID:g189206; PIDN:AAA3363.1; PID:
C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
C/Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C/Comment: This protein is thought to form a high-affinity receptor when it associates w
C/Comment: This receptor undergoes both N- and O-linked glycosylation.
C/Genetics:
A/Gene: GDNF/NGFR
A/Cross-references: GDB:120234; OMIM:162010
A/Map position: 17q21-17q22
C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 155.5; DB 1; Length 427;
Best Local Similarity 22.1%; Pred. No. 0.0026;
Matches 104; Conservative 36; Mismatches 191; Indels 139; Gaps 21;

QY 15 LLLVLGARAQGGTRSPRCADGDFHKKTGLFCRCGPAGHYLKAPC-----TEPCGNS 68
Db 16 LLLLLGLGV-SLGGAKEA---CPTGLYTHSG-ECCACNLGEGVAQPCGANQTVCEPCLD 70

QY 69 TCLVCPQDTFLAWENHNHNSCARCOACDEQASOQVALENCAS-----VADTRCGCKPGWFE 124
Db 71 ----VTFSDVVVSATP-----PKRPTCEC-----VLQSMSPAPCVCEADDAVCRCAVGYQD 116

QY 125 -----CQVSCQVSSPFFCQCLDGCALHRRHLLCRRDTCCTCLPGFY-----EH 172
Db 117 ETTGRCEACRVCESGSLVFSQ-----DKQNTVCECPCDGTYSDEANH 160

QY 173 GDGCVSCPT-----STLGGCPCERCAVCGWRQMFVQVLLAGLVVLLLGATLTYYTRHC 227
Db 161 VDFCLPCTVCEDTQRLRECTRWADAECEIPIGRWIT----- 197

QY 228 WPHKPLVTADAGMEALTP--PPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWTPG 285
Db 198 -RSTPEGSDSTAPSTQEPPEAPQDLIASTVAGVTVTWGSSQPVVTRGTTN-LIPVY 285

QY 286 PETQEAL-----CPQVTVSWDQLPSRALGFPAAAPTLSPESPAGSPAMML- 329
Db 256 CSLAAVVVGLVAYIAFKRWNSCKQKQGANSPVNTPPPEGEKLSHDSGIVSDSQSLH 315

QY 330 --QPGQ-----LYVMDAVPARR-----WKFEVTVTLGLREAEI 361
Db 316 DQOPHTQTASGQALKGDGGGLYSLP--PAKRREVEKLLNGSAGDTWRHLGELGYQPEHI 373

QY 362 EAVEVEIGRFRDQOYEMLKWRQOPAGLCAVYAALERMGLDGCVEDLRS 411
Db 374 DSFTHEACPVR-----ALLASNATQDSATLDALLAALRRRIQRADLIVESLCS 419

Search completed: March 20, 2006, 08:00:01
Job time : 29 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:11 ; Search time 110 Seconds
(without alignments)
2674.594 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLVLL.....ERMGLDGCVEDLSRLQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------|
| 1 | 2323 | 100.0 | 417 | 1 | TNR25 HUMAN |
| 2 | 2323 | 100.0 | 417 | 2 | Q5T8X6 HUMAN |
| 3 | 2312.5 | 99.5 | 418 | 2 | Q5T8X7 HUMAN |
| 4 | 2196.5 | 94.6 | 426 | 2 | Q5T8X5 HUMAN |
| 5 | 1397 | 60.1 | 413 | 2 | Q99MM1 MOUSE |
| 6 | 1255 | 54.0 | 387 | 2 | Q8VD70 MOUSE |
| 7 | 1164 | 50.1 | 253 | 2 | Q5T8X3 HUMAN |
| 8 | 1066.5 | 45.9 | 215 | 2 | Q5T8X8 HUMAN |
| 9 | 1054 | 45.4 | 277 | 2 | Q5T8X4 HUMAN |
| 10 | 1036 | 44.6 | 178 | 2 | Q5T8X2 HUMAN |
| 11 | 415 | 17.9 | 461 | 1 | TNR1A FIG |
| 12 | 406.5 | 17.5 | 440 | 2 | Q6QHF0 MOUSE |
| 13 | 405.5 | 17.5 | 440 | 2 | Q6QHF2 MUSSP |
| 14 | 404.5 | 17.4 | 440 | 2 | Q6QHF1 MOUSE |
| 15 | 404.5 | 17.4 | 454 | 1 | TNR1A MOUSE |
| 16 | 403.5 | 17.4 | 461 | 2 | Q5U1X6 RAT |
| 17 | 394.5 | 17.0 | 461 | 1 | TNR1A RAT |
| 18 | 387.5 | 16.7 | 471 | 1 | TNR1A BOVIN |
| 19 | 374 | 16.1 | 455 | 1 | TNR1A HUMAN |
| 20 | 365 | 15.7 | 446 | 2 | Q95ND3 FELCA |
| 21 | 323.5 | 13.9 | 427 | 2 | Q5ZJG1 CHICK |
| 22 | 293.5 | 12.6 | 386 | 2 | Q4SND9 TETNG |
| 23 | 247.5 | 10.7 | 332 | 1 | TNR6 FIG |
| 24 | 241.5 | 10.4 | 302 | 2 | Q4SNE8 TETNG |
| 25 | 226 | 9.7 | 319 | 2 | Q9TV79 RABIT |
| 26 | 224.5 | 9.7 | 313 | 2 | Q4G265 HORSE |
| 27 | 223.5 | 9.6 | 389 | 2 | Q6NUU6 BRARE |
| 28 | 221 | 9.5 | 314 | 2 | Q861W6 FELCA |
| 29 | 217.5 | 9.4 | 320 | 2 | Q9XS29 RABIT |
| 30 | 214.5 | 9.2 | 328 | 2 | Q76B99 XENLA |
| 31 | 211.5 | 9.1 | 328 | 2 | Q6GL24 XENLA |

| | | | | | | |
|----|-------|-----|-----|---|--------------|---------------------|
| 32 | 206.5 | 8.9 | 283 | 1 | TNR14 HUMAN | Q92956 homo sapien |
| 33 | 206.5 | 8.9 | 283 | 2 | Q6IB95 HUMAN | Q6IB95 homo sapien |
| 34 | 205 | 8.8 | 438 | 2 | Q9DFV0 BRARE | Q9DFV0 brachydanio |
| 35 | 203.5 | 8.8 | 368 | 2 | Q57408 MELGA | Q57408 melesgris g |
| 36 | 203.5 | 8.8 | 440 | 1 | TR10B HUMAN | Q14763 homo sapien |
| 37 | 203.5 | 8.8 | 440 | 2 | Q6FH58 HUMAN | Q6FH58 homo sapien |
| 38 | 200.5 | 8.6 | 283 | 2 | Q9XS28 CERAE | Q9XS28 cercopithec |
| 39 | 200 | 8.6 | 381 | 1 | TR10B MOUSE | Q9QZM4 mus musculus |
| 40 | 199.5 | 8.6 | 335 | 1 | TNR6 HUMAN | P25445 homo sapien |
| 41 | 199.5 | 8.6 | 335 | 2 | Q6ICT6 HUMAN | Q6ICT6 homo sapien |
| 42 | 199.5 | 8.6 | 335 | 2 | Q5T9P1 HUMAN | Q5T9P1 homo sapien |
| 43 | 199.5 | 8.6 | 362 | 2 | Q59F08 HUMAN | Q59F08 homo sapien |
| 44 | 199.5 | 8.6 | 368 | 2 | Q9IAR7 CHICK | Q9IAR7 gallus gall |
| 45 | 198 | 8.5 | 189 | 2 | Q95185 FELCA | Q95185 felis silve |

ALIGNMENTS

RESULT 1

| | | | | |
|----|--|-----------|------|---------|
| ID | TNR25 HUMAN | STANDARD; | PRT; | 417 AA. |
| AC | Q93038; Q00275; Q00277; Q00278; Q00279; Q00280; Q14865; | | | |
| AC | Q14866; P78507; P78515; Q92983; Q93036; Q93037; Q99722; Q99830; | | | |
| AC | Q99831; Q9BY86; Q9UM80; Q9UM81; Q9UM85; | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) | | | |
| DE | Tumor necrosis factor receptor superfamily member 25 precursor (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis inducing receptor AIR) (Apo-3) (lymphocyte associated receptor of death) (LARD). | | | |
| GN | Name=TNRSP25; Synonyms=APO3, DDR3, DR3, TNFRSF12, WSL, WSL1; | | | |
| GN | ORFNames=UNQ455(ORF0779); | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; | | | |
| OC | Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | NUCLEOTIDE SEQUENCE (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS. | | | |
| RC | TISSUE=Lymphoid; | | | |
| RX | MEDLINE=97088617; PubMed=8934525; DOI=10.1038/384372a0; | | | |
| RA | Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.; | | | |
| RT | "A death-domain-containing receptor that mediates apoptosis."; | | | |
| RL | Nature 384:372-375 (1996). | | | |
| RN | [2] | | | |
| RP | NUCLEOTIDE SEQUENCE (ISOFORM 1). | | | |
| RC | TISSUE=Umbilical vein endothelial cell; | | | |
| RX | MEDLINE=97081063; PubMed=8875942; DOI=10.1126/science.274.5289.990; | | | |
| RA | Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M., Duan D.R., King L., Gentz R., Ni J., Dixit V.M.; | | | |
| RT | "Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95."; | | | |
| RL | Science 274:990-992 (1996). | | | |
| RN | [3] | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | |
| RA | Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.; | | | |
| RL | Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [4] | | | |
| RP | NUCLEOTIDE SEQUENCE (ISOFORM 1). | | | |
| RC | TISSUE=Heart; | | | |
| RX | MEDLINE=97148200; PubMed=8994832; DOI=10.1016/S0960-9822(02)70791-4; | | | |
| RA | Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Ashkenazi A.; | | | |
| RT | "Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B."; | | | |
| RL | Curr. Biol. 6:1669-1676 (1996). | | | |
| RN | [5] | | | |
| RP | NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10). | | | |
| RX | MEDLINE=97272273; PubMed=9114039; DOI=10.1073/pnas.94.9.4615; | | | |

RA Scream G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing."; [\[6\]](#)
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 11 AND 12).
RX MEDLINE=98113360; PubMed=9446802; DOI=10.1006/bbrc.1997.7948;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas."; [\[7\]](#)
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
RN [7]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT GLY-159.
RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seahagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."; [\[9\]](#)
RL Genome Res. 13:2265-2270(2003).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLN-23; GLY-159 AND
RP ARG-254.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA [URL: <http://egp.gs.washington.edu>].";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE OF 4-417.
RC TISSUE=Brain, and Fetal lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA Browning J.L., Macdonald H.R., Tschopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology to
RT tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 7-417.
RC TISSUE=Brain;
RA Chaudhary P.M., Hood L.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [12]
RP INTERACTION WITH BAG4.
RX MEDLINE=99115917; PubMed=9915703; DOI=10.1126/science.283.5401.543;
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
RT death domains."; [\[13\]](#)
RL Science 283:543-546(1999).
RN [13]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance."; [\[14\]](#)
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
CC with the adapter TRADD. Mediates activation of NF-kappa-B and

induces apoptosis. May play a role in regulating lymphocyte
homeostasis.
-1- SUBUNIT: Homodimer. Interacts strongly via the death domains with
TNFRSF1 and TRADD to activate at least two distinct signaling
cascades, apoptosis and NF-kappa-B signaling. Interacts with BAG4.
-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
(Potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=12;
Name=1; Synonyms=WSL-1, LARD-1A;
IsoId=Q93038-1; Sequence=Displayed;
Name=2; Synonyms=LARD-1B;
IsoId=Q93038-2; Sequence=VSP_006504;
Name=3; Synonyms=WSL-S1, LARD-3;
IsoId=Q93038-3; Sequence=VSP_006497, VSP_006498;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=4; Synonyms=WSL-S2, LARD-2;
IsoId=Q93038-4; Sequence=VSP_006501, VSP_006502;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=5; Synonyms=LARD-4, LARD-11;
IsoId=Q93038-5; Sequence=VSP_006495;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=6; Synonyms=LARD-5;
IsoId=Q93038-6; Sequence=VSP_006491, VSP_006495;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=7; Synonyms=LARD-6;
IsoId=Q93038-7; Sequence=VSP_006491, VSP_006493, VSP_006494;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=8; Synonyms=LARD-7;
IsoId=Q93038-8; Sequence=VSP_006492;
Name=9; Synonyms=LARD-8;
IsoId=Q93038-9; Sequence=VSP_006491;
Name=10; Synonyms=LARD-9;
IsoId=Q93038-10; Sequence=VSP_006503;
Name=11; Synonyms=Beta;
IsoId=Q93038-11; Sequence=VSP_006496;
Name=12; Synonyms=Beta soluble;
IsoId=Q93038-12; Sequence=VSP_006499, VSP_006500;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
-1- TISSUE SPECIFICITY: Abundantly expressed in thymocytes and
lymphocytes. Detected in lymphocyte-rich tissues such as thymus,
colon, intestine, and spleen. Also found in the prostate.
-1- PTM: Glycosylated (Probable).
-1- SIMILARITY: Contains 1 death domain.
-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
-1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
residue instead of arginine.

This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; Y09392; CAA70561.1; -; mRNA.
EMBL; Y09392; CAA70559.1; -; mRNA.
EMBL; Y09392; CAA70560.1; -; mRNA.
EMBL; U72763; AAC50819.1; -; mRNA.
EMBL; U83599; AAB41434.1; -; Genomic DNA.
EMBL; U83600; AAB41435.1; -; Genomic DNA.
EMBL; U78029; AAB40918.1; -; mRNA.
EMBL; U74611; AAB39714.1; -; mRNA.
EMBL; U94501; AAC51306.1; -; mRNA.
EMBL; U94504; AAC51309.1; -; mRNA.
EMBL; U94502; AAC51307.1; -; mRNA.
EMBL; U94503; AAC51308.1; -; mRNA.


```
Db 301 WDQLPSRALGPAAAPTLLSPSPAGSPAMVLQPGQLYDVMADVARRWKEFVRTJGLREA 360
Qy 360 EIEAVEVEIGRFRDQOQYEMLKRWRQOQPAGLGAVYAALERMGLDGCVEDLRSR 417
Db 361 EIEAVEVEIGRFRDQOQYEMLKRWRQOQPAGLGAVYAALERMGLDGCVEDLRSR 418

RESULT 4
Q5T8X5_HUMAN
ID Q5T8X5_HUMAN PRELIMINARY; PRT; 426 AA.
AC Q5T8X5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 25.
GN Name=TNFRSF25; ORFNames=RP4-650H14.2-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gluthero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL158217; CA122155.1; -; Genomic DNA.
DR GO: GO:000515; F:protein binding; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; Death; 1.
DR Pfam: PF00020; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS0017; DEATH DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR KX Receptor.
SQ SEQUENCE 426 AA; 45927 MW; 292A9B2899F3AE1F CRC64;

Query Match 94.68; Score 2196.5; DB 2; Length 426;
Best Local Similarity 94.68; Pred. No. 4.5e-144;
Matches 403; Conservative 3; Mismatches 11; Indels 9; Gaps 3;

Qy 1 MEQRPRCAVAALLLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRCAVAALLLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASVADTRCGCKPG 120

Qy 121 WFVECVQSVSSPFYCPCLDCGALHRTLLCSRRDTCGCLPGFHEHGDGVCSCP 180
Db 121 WFVECVQSVSSPFYCPCLDCGALHRTLLCSRRDTCGCLPGFHEHGDGVCSCP 180

Qy 181 T--STLGSCEPERCA-----AVCCWR-QMFVQVLLAGLVVPLLGATLTYYTRHCWPHK 231
Db 181 TTPPSLAGAPGAVQSAVPLSVAGRGVGVFVQVLLAGLVVPLLGATLTYYTRHCWPHK 240

Qy 232 PLVTADAGMEALTPPPATHLSPLDSAHTLAPPDSSEKI CTVOLVNSWTPGYPTQEA 291
Db 241 PLVTADAGMEALTPPPATHLSPLDSAHTLAPPDSSEKI CTVOLVNSWTPGYPTQEA 300

Qy 292 LCPQVTSWDLPSRALGPAAAPTLLSPSPAGSPAMVLQPGQLYDVMADVARRWKEFV 351
Db 301 LCPQVTSWDLPSRALGPAAAPTLLSPSPAGSPAMVLQPGQLYDVMADVARRWKEFV 360

Qy 352 RTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQPAGLGAVYAALERMGLDGCVEDLRS 411
Db 361 RTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQPAGLGAVYAALERMGLDGCVEDLRS 420

RESULT 5
Q99MM1_MOUSE
ID Q99MM1_MOUSE PRELIMINARY; PRT; 413 AA.
AC Q99MM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE WSL-1-like protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=129/Sv;
RL MEDLINE=21158384; PubMed=11261933; DOI=10.1007/s002510000290;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT gene.";
RL Immunogenetics 53:59-63 (2001).
DR EMBL: AF329969; AAK11256.1; -; mRNA.
DR HSP: P19438; IICH.
DR Ensembl: ENSMUSG00000024793; Mus musculus.
DR MGI: MGI:1934667; Tnfrsf25.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR000488; Death.
DR InterPro: IPR011029; DEATH like.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; Death; 1.
DR Pfam: PF00020; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABABF CRC64;

Query Match 60.18; Score 1397; DB 2; Length 413;
Best Local Similarity 62.98; Pred. No. 1.1e-88;
Matches 270; Conservative 28; Mismatches 103; Indels 28; Gaps 7;

Qy 1 MEQRPRCAVAALLLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCP 52
Db 1 MEARLURGCVVBEPLFLPLLLLLLLLLLGGQGGG-MSGRCDCASESQKRGPFCCRGCP 59

Qy 53 AGHYLKPCTPECGNSTCLVCPQDTFLAWENHNSECRCQACDEQASQVALENCASVAD 112
Db 60 KGHYKAPCAEPCGNSCTCLPCPSDTFLTRDNHFKDCTRCQVCEALQVTLNCSAKSD 119

Qy 113 TRCGKPGFWFVECVQSVSSPFYCPCLDCGALHRTLLCSRRDTCGT---CLPGF 169
Db 120 THCGCSGWCVCDSFVPCGKSSPFCVPCGATTPVH-----EAPTRPCLPGF 167

Qy 170 YEHGDGVCVCSPTSTLGSCEPERCAVCGWRQVFWVQVLLAGLVVPLLGATLTYYRHCWP 229
Db 168 YIRGNDCTCPTGSSVCPKACTAVCGWKNQVFWVQVLLG---VAFLEGALICAYCRWP 224

Qy 230 HKPLVTADAGMEALTPPPATHLSPLDSAHTLAPPDSSEKIC-TVOLVNSWTPGYPT 288
Db 230 HKPLVTADAGMEALTPPPATHLSPLDSAHTLAPPDSSEKIC-TVOLVNSWTPGYPT 288
```

225 CKAVVTADTAGTETPLASPTAHLSASDSTHLLAPPSTGKICTTTLVQVGNNTPLGSLQ 284
 289 QEALCPQVTSWDQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWK 348
 285 QEVVCCQASQPDQLPNRTLTGTPSLPSPAPPAGSFAAVLQPGPOLYDMDAVPARRWK 344
 349 EFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRQOQAGLGAIVAAALERMGLDGCVD 408
 345 EFVRTLGLREAEIEAVEVEICFRDQOQYEMLKRQOQAGLGAIVAAALERMGLDGCVD 404
 409 LRSRLQGP 417
 405 LRSRLQGP 413

RESULT 6

Q8VD70_MOUSE PRELIMINARY; PRT; 387 AA.
 AC Q8VD70;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tnfrsf25 protein.
 GN Name=Tnfrsf25;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zerborg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Salivary gland;

RA Strausberg R.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC017526; AAH17526.1; -, mRNA.

DR HSSP; P19438; 11CH.

DR Ensembl; ENSMUSG00000024793; Mus musculus.

DR MGI; MGI:1934667; Tnfrsf25.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR InterPro; IPR000488; Death.

DR InterPro; IPR011029; DEATH like.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR001368; TNFR_c6.

DR Pfam; PF00531; Death; 1.

DR Pfam; PF00020; TNFR_c6; 1.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
 DR PROSITE; PS00520; TNFR_NGFR_1; UNKNOWN 1.
 DR PROSITE; PS00502; TNFR_NGFR_2; 1.
 SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;
 Query Match 54.0%; Score 1255; DB 2; Length 387;
 Best Local Similarity 57.7%; Pred. No. 7.1e-79;
 Matches 248; Conservative 26; Mismatches 92; Indels 64; Gaps 6;
 QY 2 EQRPRGCAVAAA-----LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFC 48
 DB 8 ERSPPGAATPGSTARVLQPLFLPLLLLLLLGGGGGG--MSGRCDCASESQRYPFFCC 66
 QY 49 RGCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDQASQVALENCS 108
 DB 67 RGCPRGHTYMKAPCAEPCGNSTCLPCFSDTFLTRDNHFKDCTRCQVCDSEALQVLENCS 126
 QY 109 AVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCDCLGALHRRHRLCSRDDTCGTCPLG 168
 DB 127 AKSDTHCGCGQGWCVDCSTPCGKSPFCVCGATTPTVH----- 166
 QY 169 FYEHGDCVSCPTSTLGSCTPCERCAAVCGWRQWVQVLLAGLVVPLLLGATLTYYRHCW 228
 DB 167 -----EAPT-----PLFWVQVLLG---VAFLLGAILCAVCRWQ 197
 QY 229 PHKPLVTADAGMEALTPPPATHLSPLDSAHLLAPPDSEKIC-TVQLVGNSTWTPGYPE 287
 DB 198 PKAVVVTADTAGTETLASPTAHLSASDSTHLLAPPSTGKICTTTLVQVGNNTPLGSLQ 257
 QY 288 TQALCPQVTSWDQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRW 347
 DB 258 TQEVVCCQASQPDQLPNRTLTGTPSLPSPAPPAGSFAAVLQPGPOLYDMDAVPARRW 317
 QY 348 KEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRQOQAGLGAIVAAALERMGLDGCVE 407
 DB 318 KEFVRTLGLREAEIEAVEVEICFRDQOQYEMLKRQOQAGLGAIVAAALERMGLDGCVE 377
 QY 408 DLRSRLQGP 417
 DB 378 DLRSRLQGP 387
 RESULT 7
 Q5T8X3_HUMAN PRELIMINARY; PRT; 253 AA.
 ID Q5T8X3_HUMAN PRELIMINARY;
 AC Q5T8X3;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 25.
 GN Name=TNFRSF25; ORFNames=RP4-650H14.2-003;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Glithero R.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL158217; CAI22157.1; -, Genomic DNA.
 DR Ensembl; ENSG00000171680; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR008063; Fas_receptor.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 1.
 DR SMART; PRO1680; FASRECEPTOR.
 DR SMART; SM00208; TNFR; 2.


```
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B68E9292 CRC64;

Query Match 50.1%; Score 1164; DB 2; Length 253;
Best Local Similarity 99.0%; Pred. No. 9.3e-73;
Matches 200; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQRPRCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
QY 181 TSTLGSCPERRCAAVCGWRQFW 202
DB 181 TSTLGSCPERRCAAVCGWRQSRW 202

RESULT 8
Q578X8_HUMAN
ID Q578X8_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q578X8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Name=TNFRSF25; ORFNames=RP4-650H14.2-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158217; CAI22152.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
KW Receptor.
SQ SEQUENCE 277 AA; 29111 MW; 3D19F3B847BFC093 CRC64;

Query Match 45.4%; Score 1054; DB 2; Length 277;
Best Local Similarity 72.6%; Pred. No. 4.3e-65;
Matches 204; Conservative 5; Mismatches 32; Indels 40; Gaps 8;

QY 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
QY 181 T--STLGSCP-----ERCAAVCGWR--OMFVQVLLAGLVVPLLLGATLTY 222
DB 181 TTPPSLAGAPWGAQVAVPLSVAGRVGGVGLGRVGEIGWTE----GRRV--RRGATT-- 232
QY 223 TYRHGCPHKLPL---VTADAGMEALTPPPA-----THLSPL 255
DB 233 -----QHPFAAFVLGPGAPGWPGPPPAWGHGPDHLHPPL 267

RESULT 10
Q578X2_HUMAN
ID Q578X2_HUMAN PRELIMINARY; PRT; 178 AA.
AC Q578X2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Name=TNFRSF25; ORFNames=RP4-650H14.2-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B68E9292 CRC64;

Query Match 50.1%; Score 1164; DB 2; Length 253;
Best Local Similarity 99.0%; Pred. No. 9.3e-73;
Matches 200; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQRPRCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCPLPGFYEHGDCGVSCP 180
QY 181 TSTLGSCPERRCAAVCGWRQFW 202
DB 181 TSTLGSCPERRCAAVCGWRQSRW 202

RESULT 8
Q578X8_HUMAN
ID Q578X8_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q578X8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Name=TNFRSF25; ORFNames=RP4-650H14.2-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158217; CAI22152.1; -; Genomic_DNA.
DR Ensemble; ENSG00000171680; Homo sapiens.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR Pfam; PF00531; Death.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor.
FT NON TER 1
FT NON TER 215
FT NON TER 215
SQ SEQUENCE 215 AA; 23566 MW; 6567A5D82FF62B93 CRC64;

Query Match 45.9%; Score 1066.5; DB 2; Length 215;
Best Local Similarity 99.0%; Pred. No. 4.5e-66;
Matches 201; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 200 MFVQVLLAGLVVPLLLGATLTYTYRHGCPHKLPLVTADAGMEALTPPPATHLSPLDSAH 259
DB 14 VFVQVLLAGLVVPLLLGATLTYTYRHGCPHKLPLVT-DEAGMEALTPPPATHLSPLDSAH 72
QY 260 TLLAPDSSEKICTVLQVNSWTFPGYPETQEQALCPQVTSWQDLPRLALGPAAPTLSPE 319
DB 73 TLLAPDSSEKICTVLQVNSWTFPGYPETQEQALCPQVTSWQDLPRLALGPAAPTLSPE 132
QY 320 SPAGSPAMMLQPGPOLYDVMDVAPARRWKKEFVTLGLREAEIABEVEIGRFDQOYEML 379
```

101 RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4. Constitutively associated with TRPC4AP (By similarity).

102 -1- SUBCELLULAR LOCATION: Type I membrane protein.

103 -1- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-terminal region containing the death domain are involved in the interaction with TRPC4AP (By similarity).

104 -1- SIMILARITY: Contains 1 death domain.

105 -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

106 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

107 EMBL; U19994; AAC48499.1; -, mRNA.

108 DR PIR; JC4302; JC4302.

109 DR HSP; P19438; IICH.

110 DR SMR; P50555; 362-447.

111 DR InterPro; IPR000488; Death.

112 DR InterPro; IPR011029; DEATH-like.

113 DR InterPro; IPR001368; TNFR_c6.

114 DR Pfam; PF00531; Death; 1.

115 DR Pfam; PF00020; TNFR_c6; 3.

116 DR SMART; SM00208; TNFR; 4.

117 DR PROSITE; PSS0017; DEATH DOMAIN; 1.

118 DR PROSITE; PSS00652; TNFR_NGFR_1; 3.

119 DR PROSITE; PSS0050; TNFR_NGFR_2; 2.

120 KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

121 FT SIGNAL 1 21 Potential.

122 FT CHAIN 22 461 Tumor necrosis factor receptor superfamily member 1A. Extracellular (Potential).

123 FT TOPO_DOM 22 210 Potential.

124 FT TRANSMEM 211 233 Potential.

125 FT TOPO_DOM 234 461 Cytoplasmic (Potential).

126 FT REPEAT 43 82 TNFR-Cys 1.

127 FT REPEAT 83 125 TNFR-Cys 2.

128 FT REPEAT 126 166 TNFR-Cys 3.

129 FT REPEAT 167 195 TNFR-Cys 4.

130 FT DOMAIN 340 447 Death.

131 FT REGION 340 350 N-SMase activation domain (NSD).

132 FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).

133 FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).

134 FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).

135 FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).

136 FT DISULFID 44 58 By similarity.

137 FT DISULFID 59 72 By similarity.

138 FT DISULFID 62 81 By similarity.

139 FT DISULFID 84 99 By similarity.

140 FT DISULFID 102 117 By similarity.

141 FT DISULFID 105 125 By similarity.

142 FT DISULFID 127 143 By similarity.

143 FT DISULFID 146 158 By similarity.

144 FT DISULFID 149 166 By similarity.

145 FT DISULFID 168 179 By similarity.

146 FT DISULFID 182 194 By similarity.

147 FT DISULFID 185 190 By similarity.

148 SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

149 Query Match 17.9%; Score 415; DB 1; Length 461;

150 Best Local Similarity 30.5%; Pred. No. 1.4e-20;

151 Matches 140; Conservative 44; Mismatches 20; Indels 74; Gaps 18;

152 QY 11 VAAALLLVLAGAQAQ-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCT 62

153 DB 14 VLRALLVDVYVAGVHGLVLPDREKRESLCPOGKYSHPNQNSICTCKCHKGYLHNDCL 73

154 QY 63 EPCGNSTCLVCPQDTFLAWNHNNHNSCARQACDQASQVALENCASAVADTRCGCKPGWF 122

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

201

202

203

204

205

206

207

208

209

210

211

212

213

214

215

216

217

218

219

220

221

222

223

224

225

226

227

228

229

230

231

232

233

234

235

236

237

238

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

255

256

257

258

259

260

261

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

314

315

316

317

318

319

320

321

322

323

324

325

326

327

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

508

509

510

511

512

513

514

515

516

517

518

519

520

521

522

523

524

525

526

527

528

529

530

531

532

533

534

535

536

537

538

539

540

541

542

543

544

545

546

547

548

549

550

551

552

553

554

555

556

557

558

559

560

561

562

563

564

565

566

567

568

569

570

571

572

573

574

575

576

577

578

579

580

581

582

583

584

585

586

587

588

589

590

591

592

593

594

595

596

597

598

599

600

601

602

603

604

605

606

607

608

609

610

611

612

613

614

615

616

617

618

619

620

621

622

623

624

625

626

627

628

629

630

631

632

633

634

635

636

637

638

639

640

641

642

643

644

645

646

647

648

649

650

651

652

653

654

655

656

657

658

659

660

661

662

663

664

665

666

667

668

669

670

671

672

673

674

675

676

677

678

679

680

681

682

683

684

685

686

687

688

689

690

691

692

693

694

695

696

697

698

699

700

701

702

703

704

705

706

707

708

709

710

711

712

713

714

715

716

717

718

719

720

721

722

723

724

725

726

727

728

729

730

731

732

733

734

735

736

737

738

739

740

741

742

743

744

745

746

747

748

749

750

751

752

753

754

755

756

757

758

759

760

761

762

763

764

765

766

767

768

769

770

771

772

773

774

775

776

777

778

779

780

781

782

783

784

785

786

787

788

789

790

791

792

793

794

795

796

797

798

799

800

801

802

803

804

805

806

807

808

809

810

811

812

813

814

815

816

817

818

819

820

821

822

823

824

825

826

827

828

829

830

831

832

833

834

835

836

837

838

839

840

841

842

843

844

845

846

847

848

849

850

851

852

853

854

855

856

857

858

859

860

861

862

863

864

865

866

867

868

869

870

871

872

873

874

875

876

877

878

879

880

881

882

883

884

885

886

887

888

889

890

891

892

893

894

895

896

897

898

899

900

901

902

903

904

905

906

907

908

909

910

911

912

913

914

915

916

917

918

919

920

921

922

923

924

925

926

927

928

929

930

931

932

933

934

935

936

937

938

939

940

941

942

943

944

945

946

947

948

949

950

951

952

953

954

955

956

957

958

959

960

961

962

963

964

965

966

967

968

969

970

971

972

973

974

975

976

977

978

979

980

981

982

983

984

985

986

987

988

989

990

991

992

993

994

995

996

997

998

999

1000

74 GGLDTCDECDNGTTFASEN-HLTQCLSCSKCRSEMSQVEISPTCTVDRDTCVGCCKKN-- 130

123 VECQVSQCVSSSPFFCQPCLCDGALHRRHLLC--SRRTDCGCTCLPGFYEHGDCGVCSCTP 181

131 ---QYRKWSETLFQCLNCSLCP--NGTVQLPCLEKQDITC-NCHSGFFLRDKCEKVCVCVN 184

182 STLGCSPERCAAVCGWRQMP-----WVOVLGALVPLLLGATLTYTYRHCHWPH--- 230

185 CKNADCKNLCPATSETRNDFOQTGTVLLPLVIFPGLCLAFFLVGLGACRYQRWKPKLYS 244

231 -----KPIATADEAGMEALTPPPATHLSPLD--SAHTLLAPPDSSSEKICTV 274

245 IICGKSTPVKEGEPEPLATAPSG-----PITTFSPISPSPTTTFSPVSFSPISPP 297

275 QLVGNSWT---PGYPTETQALCPQVWSDQLPSRALGPAAATPLSP-----ESPAG 323

298 TTTPCOWSNIKVTSPPKAIAPPPQAG-----PILPMPPASTVPVPLPKWGGSAHSHS 352

324 SPAMMLQGP-OLYDVMDAVPAREKFEVFTLGLREAEIEAVEVEIGR-FRDOQYEMLRK 381

353 APAQLADADPATLYAVVDGVPPTWKFEVFRVLGSEHEIERLELQNGRCLREAQYSLMAE 412

382 WRQ---QQPAGLGA VYAALERWGLDGCVEDLRSLQRGP 417

413 WRRYTSRREATLELGSVLRDMDLLGCLDTEAL-RGP 450

```

RESULT 12
Q6QHFO_MOUSE
ID ID Q6QHFO_MOUSE PRELIMINARY; PRT; 440 AA.
AC Q6QHFO;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Names=Tnf1rfla;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAN=C57BL/6JICO; TISSUE=Liver;
RA SraeJens J., Wleolockx B., Puimege L., Vandenaesle A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV541590; AAS48429.1; -; mRNA.
DR SNR; Q6QHFO; 35-191, 351-435.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; P:cell death; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.

```

```

FT  NON_TER  440  440
SQ  SEQUENCE  440  AA;  48639  MW;  D343ED449B260188  CRC64;

Query Match      17.5%;  Score 406.5;  DB 2;  Length 440;
Best Local Similarity 27.2%;  Pred. No. 5.1e-20;
Matches 127;  Conservative 56;  Mismatches 191;  Indels 93;  Gaps 18;

QY  11  VAAALLVLLGARAAQGGT-----RSPRCDGAGDFHKKIGLFCRCGCGPAGHYLKA  59
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   5  LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVSHKNNSTCTCTCKHGTYLVS  64

QY  60  PCTEPCGNSTCLVCPDPTFLAWENHNSCARCOACDBQASQVALENCNSAVADTRCGCKP  119
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   65  DCPSPGRDVTCRECEKGTFTASQNYLR-QCLSKCTCRKEMSQVEISPCQADKDTVCCK-  122

QY  120  GWFVEQVQSCVSSSPFYCQPCLDCCGALHRRHLLCSRDDTCGTCLPGFYEHGDCGVSC  179
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   123  ----ENQFQYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLESECVPC  176

QY  180  PTSTLGSCLP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLGLGATITVY  224
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   177  ----SHCKNVECKMLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY  231

QY  225  RHCLP-----HKPLVTADEAGMEALTPPPATHLSPLSAHTLL-----APPSSEK  270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   232  PRWRPEYISIIICDPVPVKEEKAGKGLTPAPSPAFSTGCFNPTLGFSTPGFSPVSSTP  291

QY  271  ICTVQLVGNW-----TPGY-PETQEALC---POVTWMDQLPSPRALGPAAAP  314
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   292  ISPI-FGPNWNHXPVPVSEVPTQAGADLLYESLCFVPAPTSQKVED-----  338

QY  315  TLPSPSPAGSPAMMQLQPOLYDMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD  373
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   339  SAHPQRPVNADLAI-----LYAVVDGVPPARWKEFMRFGLSEHEIERLEMONGRLRE  392

QY  374  QQYEMLKRRVQQOOPA---GLGAVYAALERMGDLGCVEDLRSRLQRP  417
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   393  AQYSMLEAWRRRTPRHEDTLEVVGLVSLKMNLAGCLNILEAL-RNP  438

RESULT 13
Q6QH2 MUSSP
ID  ID  Q6QH2 MUSSP PRELIMINARY;  PRT;  440  AA.
AC  Q6QH2;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  TNF receptor superfamily, member 1A (Fragment).
GN  Names=TNfrsfla;
OS  Mus spretus (Western wild mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Murinae; Mus.
NCBI_TaxID=10096;
[1]
NUCLEOTIDE SEQUENCES.
STRAN=SPRET/EI;  TISSUE=Liver;
RC  Staelens J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
RL  Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
DR  ENBL; AY541588; AAS48427.1; -; mRNA.
DR  SMR; Q6QH2; 35-191, 351-435.
DR  CO; GO:0016021; C.integral to membrane; IEA.
DR  CO; GO:0005515; P.protein binding; IEA.
DR  CO; GO:0004872; F.receptor activity; IEA.
DR  CO; GO:0006915; P.apoptosis; IEA.
DR  CO; GO:0007165; P.signal transduction; IEA.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR006209; EGF like.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; Death; 1.
DR  Pfam; PF00020; TNFR_c6; 3.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 4.

```

```
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 440 440
SQ SEQUENCE 440 AA; 48688 MW; 10E7ED7D289E0143 CRC64;

Query Match 17.5%; Score 405.5; DB 2; Length 440;
Best Local Similarity 28.1%; Pred. No. 5.9e-20;
Matches 132; Conservative 56; Mismatches 184; Indels 97; Gaps 22;

QY 11 VAAALLVLLGARAQGT-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLGHIHPSGVTGLVPSLGNREKRDLSLCPQGYVHSHKNSICCTCKHGTLYVS 64
QY 60 PCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVDTRCGCKP 119
DB 65 DCPSPGRDVTVCRCCKGTFTASQNYLR-QCLSKCTCRKEMSQVEISPCQADKDTVCCK- 122
QY 120 GMFVECVQSCVSSPFYCPQCLDCGALHRHTLLCSRRDTCGTCLPGFVEHGDGCVSC 179
DB 123 -----ENQFORHLSTHFQCVDCSPC---FNGVTVPCKETQNTVCTCHAGFFLRESECVPC 176
QY 180 PTSTLGSCLP-ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYT 224
DB 177 -----SHCKKQECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLLCSFIFSLWCY 231
QY 225 RH-----CWPHPKLVTADEAGMEALTPPPATHLSPLDSAHLL-----APDSS 268
DB 232 PRWRSEVYSIICRDSVP-VKEKAG-KPLTPAPSPAPSPPTSGFNPTLGFSTPGFSPVSS 289
QY 269 EKICTVOLVNSW-----TPGY-PETQALC-----PQVTSMDQLPSRAGPAA 312
DB 290 TPISPI-FGPSNMFMPPVSEVPTQADPLLYESLCSVPAPTSVQKWD-----PA- 340
QY 313 APTLSPSPAGSPAMMLQPGPOLYDMDVAPARRWKEFVRTLGLREAEIEAVEVEIGR-F 371
DB 341 -----HPQRPNDALAI-----LYAVDGVPPARWKEFMRFMGLSEHEIERLEMQNGHCL 390
QY 372 RDQYEMLKRWQOQPA---GLGAVYAALERMGLDGVCDLRSRLQGP 417
DB 391 REAQSMLAEAWRRTPRHEDTLEVVGLVLSKMNLTGLENILEAL-RNP 438

RESULT 14
Q6QHF1 MOUSE PRELIMINARY; PRT; 440 AA.
AC Q6QHF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=Tnfrsf1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DBA/2CrlBr; TISSUE=Liver;
RA Staelens J., Wielockx B., Pulmege L., Vandenabeele A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541589; AAS48428.1; -, mRNA.
DR SRR; G6QHF1; 35-191, 351-435.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; P:cell death; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR GO; GO:0006952; P:defense response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0006693; P:prostaglandin metabolism; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 440 440
SQ SEQUENCE 440 AA; 48632 MW; 580A2D2E334612A3 CRC64;

Query Match 17.4%; Score 404.5; DB 2; Length 440;
Best Local Similarity 27.2%; Pred. No. 7e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAAALLVLLGARAQGT-----RSPRCDGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLGHIHPSGVTGLVPSLGNREKRDLSLCPQGYVHSHKNSICCTCKHGTLYVS 64
QY 60 PCTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVDTRCGCKP 119
DB 65 DCPSPGRDVTVCRCCKGTFTASQNYLR-QCLSKCTCRKEMSQVEISPCQADKDTVCCK- 122
QY 120 GMFVECVQSCVSSPFYCPQCLDCGALHRHTLLCSRRDTCGTCLPGFVEHGDGCVSC 179
DB 123 -----ENQFORHLSTHFQCVDCSPC---FNGVTVPCKETQNTVCTCHAGFFLRESECVPC 176
QY 180 PTSTLGSCLP-ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYT 224
DB 177 -----SHCKKQECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLLCSFIFSLWCY 231
QY 225 RHCPW-----HKPLVTADEAGMEALTPPPATHLSPLDSAHLL-----APDSSSEK 270
DB 232 PRWRSEVYSIICRDPVPVKEKAGKPLTPAPSPAPSPPTSGFNPTLGFSTPGFSPVSSSTP 291
QY 271 ICTVOLVNSW-----TPGY-PETQALC-----PQVTSMDQLPSRAGPAA 314
DB 292 ISPI-FGPSNMFMPPVSEVPTQADPLLYESLCSVPAPTSVQKWD----- 338
QY 315 TLPSPSPAGSPAMMLQPGPOLYDMDVAPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
DB 339 SAHPQRPNDALAI-----LYAVDGVPPARWKEFMRFMGLSEHEIERLEMQNGRCLRE 392
QY 374 QYEMLKRWQOQPA---GLGAVYAALERMGLDGVCDLRSRLQGP 417
DB 393 AQYSMLAEAWRRTPRHEDTLEVVGLVLSKMNLTGLENILEAL-RNP 438

RESULT 15
TNRIA MOUSE
ID TNRIA MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p50)
DE (TNF-R1) (TNF-R1) (p55).
GN Name=Tnfrsf1a; Synonyms=Tnfr-1, Tnfr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
```

OX NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,
 RA Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026 (1991).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissnerghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656 (1991).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92039815; PubMed=1657766; DOI=10.1007/BF00211997;
 RA Roche J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340 (1991).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94245292; PubMed=8188324; DOI=10.1007/BF00176168;
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";
 RL Immunogenetics 39:450-451 (1994).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93156721; PubMed=8381516; DOI=10.1016/0161-5890(93)90088-S;
 RA Roche J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175 (1993).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C3H/He; TISSUE=Mesenchyme;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits

CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
 CC homotrimerization. The aggregated death domains provide a novel
 CC molecular interface that interacts specifically with the death
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 CC RIP and possibly FADD, are recruited to the complex by their
 CC association with TRADD. This complex activates at least two
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4 (By similarity). Constitutively associated with
 CC TRPC4AP.
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
 CC terminal region containing the death domain are involved in the
 CC interaction with TRPC4AP.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; M60468; AAA39751.1; -; mRNA.
 CC EMBL; M59377; AAA40464.1; -; mRNA.
 CC EMBL; X59238; CAA41922.1; -; mRNA.
 CC EMBL; X57796; CAA40936.1; -; mRNA.
 CC EMBL; L26349; AAA59361.1; -; mRNA.
 CC EMBL; M76656; AAA40465.1; -; Genomic DNA.
 CC EMBL; M8067; AAA40465.1; JOINED; Genomic DNA.
 CC EMBL; M76655; AAA40465.1; JOINED; Genomic DNA.
 CC EMBL; BC004599; AAH04599.1; -; mRNA.
 CC EMBL; BC052675; AAH52675.1; -; mRNA.
 CC PIR; A38634; GQWSTI.
 CC HSPSP; P19438; IICH.
 CC SMR; P25118; 41-197, 357-441.
 CC IntAct; P25118; -
 CC Ensembl; ENSMUSG0000030341; Mus musculus.
 CC MGI; MGI:1314884; Thirifila.
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
 CC GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
 CC GO; GO:0008219; P:cell death; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
 CC GO; GO:0006952; P:defense response; IMP.
 CC GO; GO:0006954; P:inflammatory response; IMP.
 CC GO; GO:0007242; P:intracellular signaling cascade; TAS.
 CC GO; GO:0007515; P:lymph gland development; IMP.
 CC GO; GO:0006693; P:prostaglandin metabolism; TAS.
 CC InterPro; IPR000488; Death.
 CC InterPro; IPR011029; DEATH like.
 CC InterPro; IPR001368; TNFR_C6.
 CC Pfam; PF00531; Death; 1.
 CC Pfam; PF00020; TNFR_C6; 3.
 CC PROSITE; PS00017; DEATH DOMAIN; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00050; TNFR_NGFR_2; 3.
 CC Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 CC SIGNAL 1 21 Potential.
 CC CHAIN 22 454 Tumor necrosis factor receptor
 CC superfamily member 1A.
 CC TOPO_DOM 22 212 Extracellular (Potential).
 CC TRANSMEM 213 235 Potential.
 CC TOPO_DOM 236 454 Cytoplasmic (Potential).
 CC REPEAT 43 82 TNFR-Cys 1.
 CC REPEAT 83 125 TNFR-Cys 2.
 CC REPEAT 126 166 TNFR-Cys 3.
 CC REPEAT 167 196 TNFR-Cys 4.

```
FT DOMAIN 356 441 Death.
FT REGION 339 349 N-Srase activation domain (NSD).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 195 By similarity.
FT DISULFID 185 191 By similarity.
FT CONFLICT 394 394 R -> G (in Ref. 6).
SQ SEQUENCE 454 AA; 50130 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 7.2e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAALLLVILGARAQGGT-----RSRCDACAGDFHKKIGLFCRCRGPAGHYLKA 59
DB 11 LSLVLLALLGIHPSGVTGLVPSLGDREKRDLSLCPQGYVHSHKNNISCTCKCHKGYLVS 70
QY 60 PCTEPCGNSTCLVCPQDTFLAWNHNSCARCOACDEQASQVALENCNSAVADTRCGCKP 119
DB 71 DCPSPGGRDTCRECEKGTFTASQNYLR-QCLSKCTCKEMSQVEISPCQADKDTVCCK- 128
QY 120 GWFVECVQSVCSPPYCPCLDCGALHRRHLLCSRRDTCGTCPLPGFYEHGDCVCSC 179
DB 129 -----ENQFQYLSETHFQCVCSPC--FNGTVIPCKETQNTVCNCHAGFFLESECVPC 182
QY 180 PTSTLGSCP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYYT 224
DB 183 -----SHCKKNECKMLCLPPPLANVTNPQDSGTAVLLPLVILLGLLSPFISLMCRY 237
QY 225 RHCWP-----HKPLVTADAGHEALTPPPATHLSPLDSAHTLL-----APPSSEK 270
DB 238 PRWRPEVYSIICRDVPVKEEKAGKPLTAPSPAFSPTSGFNPTLGFSTFGFSFVSSTP 297
QY 271 ICTVQLVGNW-----TPGY-PETOEALC-----PQVTSWDOLPSRALGPAAP 314
DB 298 ISPI-FGPSNWHFPPVSEVVTQGADPLLYSLCSVPAPTSVQKWD----- 344
QY 315 TLPSPSPAGSPAMLPQPOLYDMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
DB 345 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFMRFMGLSEHEIERLEMONGRCIRE 398
QY 374 QQYEMLKRWQQQPA-----GLGAVVAALERGLDGCVEDLRSRLORGP 417
DB 399 AQYSMLEAWRRTRPRHEDTLEVVGLVLSKNVLAGCLNILEAL-RNP 444
```

Search completed: March 20, 2006, 08:01:09
Job time : 111 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:04 ; Search time 86 Seconds
(without alignments)
2130.476 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAAAVAAALILVLL.....ERMGLDGCVEDLRSRLQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2323 | 100.0 | 417 | 2 | Aaw31517 Death dom |
| 2 | 2323 | 100.0 | 417 | 2 | Aaw26709 Human apo |
| 3 | 2323 | 100.0 | 417 | 2 | Aaw57045 Human apo |
| 4 | 2323 | 100.0 | 417 | 2 | Aaw95538 Death dom |
| 5 | 2323 | 100.0 | 417 | 2 | Aay05743 Tumour ne |
| 6 | 2323 | 100.0 | 417 | 3 | Aab36265 Human dea |
| 7 | 2323 | 100.0 | 417 | 4 | Aab97370 Human rhe |
| 8 | 2323 | 100.0 | 417 | 5 | Aao17879 Human rhe |
| 9 | 2323 | 100.0 | 417 | 5 | Aau86139 Human PRO |
| 10 | 2323 | 100.0 | 417 | 6 | ABG73993 Human Apo |
| 11 | 2323 | 100.0 | 417 | 6 | ABU08252 Human Apo |
| 12 | 2323 | 100.0 | 417 | 6 | ABG73859 Human foe |
| 13 | 2323 | 100.0 | 417 | 6 | ABU10204 Human GEN |
| 14 | 2323 | 100.0 | 417 | 6 | ADA00738 Human GEN |
| 15 | 2323 | 100.0 | 417 | 6 | ABG73824 Human apo |
| 16 | 2323 | 100.0 | 417 | 6 | ADA49692 Human Apo |
| 17 | 2323 | 100.0 | 417 | 7 | ABW02265 Human TNF |
| 18 | 2323 | 100.0 | 417 | 7 | ADG88381 Human dea |
| 19 | 2323 | 100.0 | 417 | 7 | ADJ37305 Human tum |
| 20 | 2323 | 100.0 | 417 | 7 | ADN95869 Human BEC |
| 21 | 2323 | 100.0 | 417 | 8 | ADH34623 TNF recep |
| 22 | 2323 | 100.0 | 417 | 8 | ADG68229 Human PRO |
| 23 | 2323 | 100.0 | 417 | 8 | ADL27893 Human Dea |
| 24 | 2323 | 100.0 | 417 | 8 | ADQ16568 Human dea |

| | | | | | |
|----|--------|-------|-----|---|--------------------|
| 25 | 2323 | 100.0 | 417 | 8 | ADQ59120 Human dea |
| 26 | 2323 | 100.0 | 417 | 8 | ADU04624 Tumour ne |
| 27 | 2323 | 100.0 | 418 | 4 | Aab84941 Amino aci |
| 28 | 2323 | 100.0 | 418 | 8 | ADH50948 Human dea |
| 29 | 2323 | 100.0 | 833 | 2 | Aaw64486 Human DR3 |
| 30 | 2308.5 | 99.4 | 416 | 6 | ABG73995 Human Apo |
| 31 | 2308.5 | 99.4 | 416 | 6 | ABG73862 Human foe |
| 32 | 2306 | 99.3 | 417 | 7 | ADL15011 Human WSL |
| 33 | 2292 | 98.7 | 451 | 8 | ABM84914 Human dia |
| 34 | 2277.5 | 98.0 | 450 | 8 | ABM84915 Human dia |
| 35 | 2267 | 97.6 | 428 | 2 | Aaw31516 Death dom |
| 36 | 2267 | 97.6 | 428 | 2 | Aaw95537 Death dom |
| 37 | 2267 | 97.6 | 428 | 3 | AAB36264 Human dea |
| 38 | 2267 | 97.6 | 428 | 8 | ADG88379 Human DR3 |
| 39 | 2267 | 97.6 | 428 | 8 | ADL27891 Human Dea |
| 40 | 2196.5 | 94.6 | 426 | 9 | ADY17600 PRO polyp |
| 41 | 2179.5 | 93.8 | 426 | 3 | AAB01337 TNF recep |
| 42 | 1862 | 80.2 | 343 | 4 | AAB50918 Human PRO |
| 43 | 1404 | 60.4 | 411 | 2 | Aaw57046 Mouse apo |
| 44 | 1164 | 50.1 | 253 | 7 | ADL15009 Human WSL |
| 45 | 1052.5 | 45.3 | 218 | 7 | ADL15010 Human WSL |

ALIGNMENTS

RESULT 1

Aaw31517

ID Aaw31517 standard; protein; 417 AA.

XX

AC Aaw31517;

XX

DT 02-MAR-1998 (first entry)

XX

DE Death domain containing receptor DR3.

XX

KW Death domain containing receptor; DR3-V1; human; apoptosis; inflammation;

KW

OS NF-kappaB.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

```
PS Claim 1; Page 75-77; 108pp; English.
XX
CC This protein comprises human death domain containing receptor DR3, a
CC novel member of the tumour necrosis factor receptor family. Its amino
CC acid sequence was deduced from a cDNA clone (see AAT9427) isolated from
CC a HUVBC cDNA library. Related death domain containing receptor DR3-V1
CC (see AAW31516) has also been identified. Recombinant full-length or
CC mature DR3, or the extracellular, transmembrane, intracellular or death
CC domain of DR3 can be expressed in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated with
CC the inhibition of apoptosis, or to screen for modulator compounds.
CC Antagonists, such as antibodies raised against DR3-V1, can be used to
CC treat diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
DB 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
QY 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
DB 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300

RESULT 2
AAW26709
ID AAW26709 standard; protein; 417 AA.
XX
AC AAW26709;
XX
DT 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-3.
XX
KW Apo-3; apoptosis; human; therapy.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FT Peptide 1..24
FT /label= Sig_peptide
FT Domain 25..198
FT /note= "extracellular domain"
FT Modified-site 67
FT /note= "N-glycosylated"
FT Modified-site 106
FT /note= "N-glycosylated"
FT

Domain 199..224
/Note= "transmembrane domain"
Domain 225..417
/Note= "intracellular domain"
Domain 338..417
/Note= "death domain"

WO9737020-A1.
XX
XX
PD 09-OCT-1997.
XX
XX
PF 31-MAR-1997; 97WO-US005230.
XX
XX
PR 01-APR-1996; 96US-00625328.
XX
XX
PR 23-SEP-1996; 96US-00710802.
XX
XX
PA (GETH ) GENENTECH INC.
XX
XX
PI Ashkenazi AJ;
XX
XX
WI; 1997-503105/46.
XX
XX
N-PSDB; AAT91180.
XX
XX
Polyptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in
XX mammalian cells.
XX
XX
Claim 19; Page 46-48; 70pp; English.
XX
CC This novel polypeptide, designated Apo-3, is a protein that stimulates or
CC induces apoptotic activity in mammalian cells purposes. Its amino acid
CC sequence was deduced from a human foetal heart cDNA clone (see AAT91180).
CC The N-terminal 181 amino acids of Apo-3 are identical to the sequence of
CC another novel apoptosis polypeptide, Apo-2LI (see AAW26709). Also claimed
CC are: polypeptides comprising the extracellular or death domain of Apo-3;
CC chimeric molecules comprising Apo-3 fused to a heterologous amino acid
CC sequence; antibodies that bind to Apo-3 or its extracellular domain;
CC nucleic acids encoding the polypeptides, as well as vectors and host
CC cells; a non-human transgenic animal containing cells that express
CC nucleic acid encoding Apo-3; and a non-human knockout animal containing
CC cells having an altered Apo-3 gene. Apo-3 can be used to induce apoptosis
CC or NF-kappa-B- (NF-kB)- or JNK-mediated gene expression for therapeutic
CC purposes. Apo-3-IgG fusion proteins can be used to inhibit apoptosis or
CC NF-kB induction or JNK activation for therapeutic purposes, and can be
CC used as immunogens for anti-Apo-3- antibody production. Apo-3 or Apo-2LI
CC can also be used as assay standards. The animals can be used in drug
CC screening and development
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIQLFCCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARQACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
DB 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
```

```
QY 301 DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMQVAVPARRWKEFVRTLGLEAE 360
DB 301 DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMQVAVPARRWKEFVRTLGLEAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWQQQPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWQQQPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 3
AAW57045
ID AAW57045 standard; protein; 417 AA.
AC AAW57045;
DT 20-AUG-1998 (first entry)
XX Human apoptosis inducing receptor.
XX Apoptosis inducing receptor; AIR protein; human; cell death regulator;
XX Type I transmembrane protein; tumour cell death; autoimmune disease;
XX therapy.
XX Homo sapiens.
XX WO9814565-A1.
XX 09-APR-1998.
XX 03-OCT-1997; 97WO-US017876.
XX 04-OCT-1996; 96US-0044456P.
XX (IMMV ) IMMUNEX CORP.
XX Perkins PA;
XX WPI; 1998-240077/21.
XX N-PSDB; AAV28700.
XX DNA encoding apoptosis inducing receptor - which is Type I transmembrane
XX protein, useful for regulating cell death.
XX Claim 16; Page 28-30; 45pp; English.
XX This sequence is the human apoptosis inducing receptor (AIR) of the
XX invention. AIR is a Type I transmembrane protein, soluble forms of which
XX can be used to regulate cell death in a therapeutic setting. Soluble AIR
XX can also be used in vitro to block apoptosis or AIR-expressing cells, or
XX to screen agonists or antagonists of AIR activity. The cytoplasmic domain
XX of AIR can be used to develop assays for inhibitors of AIR-induced cell
XX death, which is useful to regulate cell death in a therapeutic setting as
XX well as in vitro. Agonists of AIR activity can be used to kill tumour
XX cells that express AIR, or T cells expressing AIR in autoimmune diseases
XX
XX Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTPECGNSTCLVCPQDTFLAWENHNSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCQCLDGLGALHRRHTRLLCSRDTDCGTC LPGFVEHGDGVSCP 180
DB 121 WFVECVQSCVSSSPFYCQCLDGLGALHRRHTRLLCSRDTDCGTC LPGFVEHGDGVSCP 180
```

```
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVLTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVLTADAG 240
QY 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNHSWTGYPETQEQALCPQVTTWSW 300
DB 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNHSWTGYPETQEQALCPQVTTWSW 300
QY 301 DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMQVAVPARRWKEFVRTLGLEAE 360
DB 301 DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMQVAVPARRWKEFVRTLGLEAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWQQQPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWQQQPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 4
AAW95538
ID AAW95538 standard; protein; 417 AA.
AC AAW95538;
DT 25-MAR-1999 (first entry)
XX Death domain containing receptor polypeptide (DR3).
XX Death domain; receptor; DR3-V1; DR3; recombinant.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..24
XX Protein 25..417
XX /note= "signal peptide"
XX /note= "mature protein"
XX JP11000170-A.
XX 06-JAN-1999.
XX 12-MAR-1997; 97JP-00057503.
XX 12-MAR-1996; 96US-0013285P.
XX 17-OCT-1996; 96US-0028711P.
XX 06-FEB-1997; 97US-0037341P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI ) UNIV MICHIGAN.
XX WPI; 1999-124390/11.
XX N-PSDB; AAX00925.
XX New death domain containing receptor and recombinant vector - optionally
XX comprising leader sequence.
XX Claim 1; Fig 3; 50pp; Japanese.
XX The invention provides nucleotide sequences encoding death domain
XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is
XX contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX the nucleic acid sequences and optionally the leader sequences are used
XX for the recombinant production of the proteins. The present sequence
XX represents the amino acid sequence of a death domain containing receptor
XX polypeptide (DR3)
XX
XX Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MEORPRCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 DB 1 MEORPRCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
 DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120
 QY 121 WFVECVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHDGCVSCP 180
 DB 121 WFVECVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHDGCVSCP 180
 QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADG 240
 DB 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADG 240
 QY 241 MEALTTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSSWTGYPETQALCPQVTWSW 300
 DB 241 MEALTTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSSWTGYPETQALCPQVTWSW 300
 QY 301 DQPSRALGPAAPTILSPSPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLGLEAE 360
 DB 301 DQPSRALGPAAPTILSPSPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLGLEAE 360
 QY 361 IEAVEVEIGRFDDQOYEMLKRWQOQPGAGLVYAALERMGLDGCVEDLRSRLQGP 417
 DB 361 IEAVEVEIGRFDDQOYEMLKRWQOQPGAGLVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 5 AAY05743

ID AAY05743 standard; protein; 417 AA.

AC AAY05743;

XX 19-JUL-1999 (first entry)

XX Tumour necrosis factor receptor TR3.

XX Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist;
 KW antagonist; screening; human; Alzheimer's disease; AIDS; cancer;
 KW inflammation; arthritis; septicemia; autoimmune disease; psoriasis;
 KW inflammatory bowel disease; infection; transplant rejection;
 KW graft versus host disease; transfusion; stroke; ischaemia;
 KW acute respiratory disease syndrome; restenosis; brain injury;
 KW bone disease; atherosclerosis; therapy.

XX Homo sapiens.

XX EP911633-A1.

XX 28-APR-1999.

XX 02-OCT-1998; 98EP-00203332.

XX 08-OCT-1997; 97US-0061334P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX McDonnell PC, Young PR, Zou J;

XX WPI; 1999-246560/21.

XX Identifying agonists and antagonists of tumor necrosis factor related
 PT receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of
 PT cancer, AIDS, Alzheimer's disease, bone disease etc.

XX Disclosure; Page 12-13; 23pp; English.

XX The present sequence represents tumour necrosis factor receptor (TNFR)
 CC TR31, also known as DR3, Apo3, WSL-1 or LARD. The invention relates to
 CC TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their
 CC ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed

CC methods of identifying agonists and antagonists, i.e. compounds that bind
 CC to the receptors or ligand, and which activate (agonist) or inhibit
 CC activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for
 CC identifying agonists, antagonists, ligands, receptors, substrates,
 CC enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The
 CC agonists and antagonists are useful for treatment of chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune disease e.g.
 CC inflammatory bowel disease, psoriasis, transplant rejection, graft versus
 CC host disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis, Alzheimer's disease,
 CC etc., caused by imbalance of TR1, TR3, TR5 or TL3
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.5e-161;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

DB 1 MEORPRCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120

DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCDQASQVALENCASAVADTRCGCKPG 120

QY 121 WFVECVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHDGCVSCP 180

DB 121 WFVECVQSVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHDGCVSCP 180

QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADG 240

DB 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCWPKPLVTADG 240

QY 241 MEALTTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSSWTGYPETQALCPQVTWSW 300

DB 241 MEALTTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSSWTGYPETQALCPQVTWSW 300

QY 301 DQPSRALGPAAPTILSPSPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLGLEAE 360

DB 301 DQPSRALGPAAPTILSPSPAGSPAMMLQPGPOLYDMDVAVPARRWKEFVRTLGLEAE 360

QY 361 IEAVEVEIGRFDDQOYEMLKRWQOQPGAGLVYAALERMGLDGCVEDLRSRLQGP 417

DB 361 IEAVEVEIGRFDDQOYEMLKRWQOQPGAGLVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 6 AAB36265

ID AAB36265 standard; protein; 417 AA.

XX AAB36265;

XX 20-FEB-2001 (first entry)

XX Human death domain containing receptor DR3.

XX Human; death domain containing receptor; DR3; cancer;
 KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
 KW neurodegenerative disease; angiogenesis.

XX Homo sapiens.

XX WO200064465-A1.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US010741.

XX 22-APR-1999; 99US-0130488P.

XX 28-MAY-1999; 99US-0136741P.

PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX WPI; 2000-687263/67.
DR N-PSDB; AAC68777.
XX
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent.
XX
XX Claim 1; Fig 2; 273pp; English.
XX
XX The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCTCLPGFYEHDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCTCLPGFYEHDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADAG 240
QY 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
DB 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
QY 301 DQLPSPALGFAAAPTLSPEPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360
DB 301 DQLPSPALGFAAAPTLSPEPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRKRWQQQAPAGVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGFRDQOQYEMLRKRWQQQAPAGVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 7
AAB97370
ID AAB97370 standard; protein; 417 AA.
XX AAB97370;
AC AAB97370;
XX
DT 15-AUG-2001 (first entry)
XX
XX Human rheumatoid arthritis associated transmembrane protein.

XX Rheumatoid arthritis; transmembrane protein; human.
XX Homo sapiens.
XX WO200132921-A2.
XX 10-MAY-2001.
XX 01-NOV-2000; 2000WO-JP007690.
XX 01-NOV-1999; 99JP-00310805.
XX (SHIO/) SHIOZAWA S.
XX Shiozawa S, Konishi Y;
DR WPI; 2001-308750/32.
DR N-PSDB; AAH27782.
XX
XX Diagnosing rheumatoid arthritis by probing digested human genomic DNA or
PT comparing expression of mRNA or polypeptide of a region of transmembrane
PT protein.
XX
XX Disclosure; Page 15-17; 21pp; Japanese.
XX
XX This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridising it
CC with a probe for the DNA encoding the present protein which is a
CC rheumatoid arthritis associated transmembrane protein. The method is used
CC for the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCTCLPGFYEHDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCTCLPGFYEHDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADAG 240
QY 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
DB 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
QY 301 DQLPSPALGFAAAPTLSPEPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360
DB 301 DQLPSPALGFAAAPTLSPEPAGSPAMMLQPGPOLYDVMADVAPARRWKEFVRTLGLEAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRKRWQQQAPAGVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGFRDQOQYEMLRKRWQQQAPAGVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 8
AAB97370
ID AAB97370 standard; protein; 417 AA.
XX
AC AAB97370;

XX DT 22-AUG-2002 (first entry)
XX DE Human rheumatoid arthritis associated DR3 gene related protein #1.
XX KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN WO200234912-A1.
XX PD 02-MAY-2002.
XX PF 24-OCT-2001; 2001WO-JP009313.
XX PR 24-OCT-2000; 2000JP-00324296.
XX PR 27-MAR-2001; 2001JP-00090546.
XX PR 30-MAR-2001; 2001JP-00099990.
XX (NEWI-) NEW IND RES ORG.
XX PA (SHIO/) SHIOZAWA S.
XX PI Shiozawa S, Konishi Y;
XX WPI; 2002-417132/44.
XX DR N-PSDB; AAL47186.
XX PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX PT arthritis via mutation, useful in evaluating disease onset and its
XX PT possibility and providing therapy and remedies.
XX PS Claim 2; Page 69-70; 84pp; Japanese.
XX CC The present invention relates to the human DR3 gene, which is associated
XX CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
XX CC the disease. The sequences can be used to evaluate disease onset and its
XX CC possibility and to provide therapy and remedies. The present sequence is
XX CC a protein described in the exemplification of the invention
XX SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCPCPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCPCPAGHYLKAP 60
QY 61 CTETPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTETPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQCVQCVSSPFCYCPCLDCGALHRRHTRLLCSRRDTCCTCLPGFYEHGDCGVSCP 180
DB 121 WFVEQCVQCVSSPFCYCPCLDCGALHRRHTRLLCSRRDTCCTCLPGFYEHGDCGVSCP 180
QY 181 TSTLGSQPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTTADEAG 240
DB 181 TSTLGSQPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTTADEAG 240
QY 241 MEALTTPPATLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTTWSW 300
DB 241 MEALTTPPATLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTTWSW 300
QY 301 DQLPSRALGPAAATLSPESPAGSPAMMLQPGPOLYDVMDDAVPARWKEFVRLTGLREAE 360
DB 301 DQLPSRALGPAAATLSPESPAGSPAMMLQPGPOLYDVMDDAVPARWKEFVRLTGLREAE 360
QY 361 IEAVEVEIGFRQOQYEMLRWQOQAPAGLVAYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGFRQOQYEMLRWQOQAPAGLVAYALERMGLDGCVEDLRSRLQRP 417

RESULT 9

AAU86139
ID AAU86139 standard; protein; 417 AA.
XX AC AAU86139;
XX DT 15-JUL-2002 (first entry)
XX DE Human PRO779 polypeptide.
XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
XX KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
XX KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
XX KW neuroprotective.
XX OS Homo sapiens.
XX PN WO200153486-A1.
XX PD 26-JUL-2001.
XX PF 11-FEB-2000; 2000WO-US003565.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 11-MAR-1999; 99US-0123972P.
XX PR 11-MAY-1999; 99US-0133459P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 22-JUN-1999; 99US-0140650P.
XX PR 22-JUN-1999; 99US-0140653P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 28-JUL-1999; 99US-0146222P.
XX PR 17-AUG-1999; 99US-0149395P.
XX PR 31-AUG-1999; 99US-0151689P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 05-JAN-2000; 2000WO-US000219.
XX (GETH) GENENTECH INC.
XX PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
XX PI Marschers SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
XX PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
XX DR N-PSDB; ABR40265.
XX PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating
XX PT benign or malignant tumors, leukemias and lymphoid malignancies,
XX PT inflammatory, angiogenic and immunologic disorders.
XX PS Claim 61; Fig 24; 302pp; English.
XX CC The present invention relates to the isolation of novel human PRO
XX CC polypeptides and the polynucleotide sequences encoding them. The PRO
XX CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
XX CC treating benign or malignant tumours (e.g. renal, kidney, bladder,
XX CC breast, etc), leukaemias and lymphoid malignancies, other disorders such
XX CC as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
XX CC stromal and blastocoele disorders, inflammatory, immune and angiogenic
XX CC disorders. The polynucleotide sequences are also useful in gene therapy.
XX CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention
XX SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECOVSOVSSSPYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFVEHGDGCVSCP 180
DB 121 WFVECOVSOVSSSPYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHSLPLDSAHNTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHSLPLDSAHNTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
QY 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWFRQQQAGLGAVYAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWFRQQQAGLGAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 10
ABG73993
ID ABG73993 standard; protein; 417 AA.
AC ABG73993;
DT 01-APR-2003 (first entry)
XX Human Apo3 protein.
XX Apo-3; human; apoptosis; monoclonal antibody; cytostatic; cancer;
KW autoimmune; inflammatory; neurodegenerative disease.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..24
FT Domain 25..198
FT Modified-site 67 /note= "Extracellular domain"
FT Modified-site 106 /note= "N glycosylated"
FT Domain 199..224 /note= "N glycosylated"
FT Domain 225..417 /note= "Transmembrane domain"
FT Region 236 /note= "Intracellular domain"
FT /note= "This Alanine is not present in the Apo3 variant
FT that is expressed in foetal heart"
XX US6469144-B1.
XX 22-OCT-2002.
XX 31-MAR-1997; 97US-00828683.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ;
XX WPI; 2003-147110/14.
DR N-PSDB; ABX15842.
XX
PT Novel isolated monoclonal antibody useful for activating or stimulating
PT apoptosis in cancer cells, comprises an antigen binding site which binds
PT to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
XX
PS Claim 1; Fig 4; 48pp; English.
XX
CC This invention relates to an isolated monoclonal antibody comprising an
CC antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)
CC polypeptide and an antibody that binds the Apo3 protein. The antibodies
CC of the invention may have cytostatic activity and may act as activators
CC or stimulators of apoptosis in cancer cells, as blockers of excessive
CC apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting
CC from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase
CC (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in
CC therapeutic purposes for activating or stimulating apoptosis in cancer
CC cells and may be used to block excessive apoptosis (for example in
CC neurodegenerative disease), or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB
CC activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody
CC may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g. ...
CC detecting Apo-2LI or Apo-3 expression in specific cells, tissues or
CC serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant
CC cell culture or natural sources. The present sequence represents the
CC human Apo3 protein which was used to generate the antibody of the
CC invention
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECOVSOVSSSPYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFVEHGDGCVSCP 180
DB 121 WFVECOVSOVSSSPYCPCLDCGALHRRHRLLCSSRDTCGTCPLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHSLPLDSAHNTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHSLPLDSAHNTLLAPPDSSEKICTVQLVGNSTWTPGYPTQALCPQVTWSW 300
QY 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWFRQQQAGLGAVYAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWFRQQQAGLGAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 11
ABU08252
ID ABU08252 standard; protein; 417 AA.
XX ABU08252;
AC ABU08252;
XX 13-MAY-2003 (first entry)
XX

| | | | | | | |
|----|----|--|----|-----|---|-----|
| XX | DE | Human Apo-3 protein. | Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCASAVADTRCGCKPG | 120 |
| XX | KW | Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS; | Qy | 121 | WFVECVQVSSPPFYCQPCDCLGALHRRHRLLCSSRDTCGTCCLPGFVHGDCVSCP | 180 |
| XX | KW | acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer; | Db | 121 | WFVECVQVSSPPFYCQPCDCLGALHRRHRLLCSSRDTCGTCCLPGFVHGDCVSCP | 180 |
| XX | KW | Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; | Qy | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVVPLLGATLTYYVHCHWPKHPLVTADEAG | 240 |
| XX | KW | retinitis pigmentosa; aplastic anaemia; cerebellar degeneration; | Db | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVVPLLGATLTYYVHCHWPKHPLVTADEAG | 240 |
| XX | KW | myocardial infarction; reperfusion injury; toxin-induced liver disease; | Qy | 241 | MEALTPPPATHLSPLDSAHTLLAPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTSW | 300 |
| XX | OS | chromosome 1q36.3; programmed cell death. | Db | 241 | MEALTPPPATHLSPLDSAHTLLAPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTSW | 300 |
| XX | OS | Homo sapiens. | Qy | 301 | DQLPSRALGPAAPPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE | 360 |
| XX | PH | Key | Db | 301 | DQLPSRALGPAAPPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE | 360 |
| XX | FT | Domain | Qy | 361 | IEAVEVEIGRFRDOQYEMLKRQOQAPAGVYVALERMLDGCVEDLRSRLQGP | 417 |
| XX | FT | 1. .198 | Db | 361 | IEAVEVEIGRFRDOQYEMLKRQOQAPAGVYVALERMLDGCVEDLRSRLQGP | 417 |
| XX | FT | /label= Extracellular domain | Qy | | | |
| XX | FT | /note= "This domain is claimed in claim 26" | Db | | | |
| XX | FT | 338. .417 | Qy | | | |
| XX | FT | /label= Death domain | Db | | | |
| XX | FT | /note= "This domain is claimed in claim 27" | Qy | | | |
| XX | FT | US2002165157-A1. | Db | | | |
| XX | FT | 07-NOV-2002. | Qy | | | |
| XX | FT | 21-FEB-2002; 2002US-00081280. | Db | | | |
| XX | FT | 01-APR-1996; 96US-0014699P. | Qy | | | |
| XX | FT | 23-SEP-1996; 96US-0026943P. | Db | | | |
| XX | FT | 31-MAR-1997; 97US-00829270. | Qy | | | |
| XX | FT | (GETH) GENENTECH INC. | Db | | | |
| XX | FT | Ashkenazi AJ; | Qy | | | |
| XX | FT | WPI; 2003-298703/29. | Db | | | |
| XX | FT | N-PSDB; ABX13179. | Qy | | | |
| XX | FT | New biologically active Apo-2LI or Apo-3 polypeptide, useful for | Db | | | |
| XX | FT | preparing a composition for treating cancer. | Qy | | | |
| XX | FT | Claim 22; Fig 4; 45pp; English. | Db | | | |
| XX | FT | The invention relates to a new isolated biologically active Apo-2LI or | Qy | | | |
| XX | FT | Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or | Db | | | |
| XX | FT | or Apo-3 appearing as ABU08251 and ABU08252. Also included are a | Qy | | | |
| XX | FT | chimeric molecule comprising the Apo-2LI fused to a heterologous amino | Db | | | |
| XX | FT | acid sequence; a dimer molecule comprising a first Apo-2LI and a second | Qy | | | |
| XX | FT | Apo-2LI; an antibody that binds to Apo-2LI or Apo-3 (or to its | Db | | | |
| XX | FT | extracellular domain sequence), an isolated nucleic acid encoding Apo-2LI | Qy | | | |
| XX | FT | or Apo-3, a vector comprising the nucleic acid, a host cell comprising | Db | | | |
| XX | FT | the vector, a method of producing Apo-2LI and a non-human (transgenic or | Qy | | | |
| XX | FT | knockout) animal that contains cells that express nucleic acid encoding | Db | | | |
| XX | FT | Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 | Qy | | | |
| XX | FT | are involved in apoptosis (programmed cell death) which is implicated in | Db | | | |
| XX | FT | AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease, | Qy | | | |
| XX | FT | Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, | Db | | | |
| XX | FT | retinitis pigmentosa, aplastic anaemia, cerebellar degeneration, | Qy | | | |
| XX | FT | myocardial infarction, reperfusion injury and toxin-induced liver | Db | | | |
| XX | FT | disease. The gene for both proteins is located on chromosome 1q36.3 Apo- | Qy | | | |
| XX | FT | 2LI and Apo-3 are also useful for preparing a composition for treating | Db | | | |
| XX | FT | cancer. The present sequence represents Apo-3 | Qy | | | |
| XX | FT | Sequence 417 AA; | Db | | | |
| XX | FT | Query Match | Qy | | | |
| XX | FT | Best Local Similarity | Db | | | |
| XX | FT | Matches 417; Conservative | Qy | | | |
| XX | FT | 0; Mismatches | Db | | | |
| XX | FT | 0; Indels | Qy | | | |
| XX | FT | 0; Gaps | Db | | | |
| XX | FT | 0; | Qy | | | |
| XX | FT | 1 MEORPRGCAVAAALLVLLGARACQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP | Db | | | |
| XX | FT | 60 | Qy | | | |
| XX | FT | 1 MEORPRGCAVAAALLVLLGARACQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP | Db | | | |
| XX | FT | 60 | Qy | | | |
| XX | FT | 61 CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCASAVADTRCGCKPG | Db | | | |
| XX | FT | 120 | Qy | | | |

Query Match 100.0%; Score 2323; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.5e-161;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAAALLVLLGARACQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Db 1 MEORPRGCAVAAALLVLLGARACQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCASAVADTRCGCKPG 120

US6462176-B1.

08-OCT-2002.

11-SEP-1997; 97US-00928069.

23-SEP-1996; 96US-0026943P.

(GETH) GENENTECH INC.

RESULT 12

ABG73859

ID ABG73859 standard; protein; 417 AA.

AC ABG73859;

DT 03-APR-2003 (first entry)

DE Human foetal heart Apo-3 protein.

OS Homo sapiens.

Key Location/Qualifiers
 Domain 1. .198 /note= "Extracellular domain. This domain is specifically claimed in claim 2 of the specification"
 Peptide 1. .24 /label= Signal_peptide
 Protein 25. .417 /note= "Mature Apo-3 protein"
 Modified-site 67 /note= "N-glycosylated"
 Modified-site 106 /note= "N-glycosylated"
 Domain 199. .224 /note= "Transmembrane domain"
 Domain 225. .417 /note= "Intracellular domain"
 Domain 338. .417 /note= "Death domain. This domain is specifically claimed in claim 3 of the specification"

Human; Apo-3; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;

nuclear factor-kappa B; NF-kappa B; Alzheimer's disease; AIDS;

tumour necrosis factor receptor; acquired immunodeficiency syndrome;

Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;

retinitis pigmentosa; cerebellar degeneration; aplastic anaemia;

myocardial infarction; stroke; reperfusion injury;

toxin-induced liver disease; cancer; lupus; herpes virus infection.

XX Ashkenazi AJ;
PI WPI: 2003-173840/17.
DR N-PSDB; ABX15464.
XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
PT mammalian cells, for generating antibodies, in affinity purification
PT techniques, and in competitive-type receptor binding assays.
XX Claim 1; Fig 8; 52pp; English.
XX The invention relates to an Apo-3 polypeptide having an extracellular
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
CC has been found to stimulate or induce apoptotic activity in mammalian
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
CC receptor (TNFR) family of polypeptides. The invention also relates to a
CC chimeric molecule comprising an extracellular domain sequence comprising
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
CC mammalian cells. Decreased levels of apoptosis has been associated with
CC conditions such as cancer, lupus, and herpes virus infection. Increased
CC levels of apoptosis are associated with diseases such as acquired
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
CC as in quantitative diagnostic assays as a control against which samples
CC containing unknown quantities of Apo-3 may be prepared, in generating
CC antibodies, as standards in assays for Apo-3, in affinity purification
CC techniques, and in competitive-type receptor binding assays. The chimeric
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
CC Apo-3 antibodies. The present sequence represents the polypeptide
CC sequence of the human Apo-3 protein present in the foetal heart
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTBPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTBPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECCQVSCVSSPFYQPCDCLGALHRRHTRLLCSRDDTCTCLPGFVEHGDGVSCP 180
DB 121 WFVECCQVSCVSSPFYQPCDCLGALHRRHTRLLCSRDDTCTCLPGFVEHGDGVSCP 180
QY 181 TSTLGSFCPCAAVCGWRQFWQVLLAGLVVPLLGATLITYRHCHWPKPLVTADEAG 240
DB 181 TSTLGSFCPCAAVCGWRQFWQVLLAGLVVPLLGATLITYRHCHWPKPLVTADEAG 240
QY 241 MEALTPTTPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
DB 241 MEALTPTTPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
QY 301 DQLPSRALGPAAPATLSPSPAGSPAMWLPQPGQVDMVDVAPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRALGPAAPATLSPSPAGSPAMWLPQPGQVDMVDVAPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQVQYEMLRWRQQQAGLGVAVYALERNMGLDGVEDLSRLQRGP 417
DB 361 IEAVEVEIGFRDQVQYEMLRWRQQQAGLGVAVYALERNMGLDGVEDLSRLQRGP 417

RESULT 13

ABU10204
ID ABU10204 standard; protein; 417 AA.
XX
AC ABU10204;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Apo-3.
XX
KW Human; Apo-3; apoptosis; gene therapy; inflammation; cancer;
KW neurodegenerative disease; immunosuppressive; tissue typing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 /label= Signal_sequence
FT Protein 25..417 /label= Mature_Apo-3
FT Domain 25..198 /label= Extracellular_domain
FT Domain 199..224 /label= Transmembrane_domain
FT Domain 225..417 /label= Intracellular_domain
FT Domain 338..417 /label= Death_domain
XX
PN US2003004313-A1.
XX
PD 02-JAN-2003.
XX
PF 28-MAR-2002; 2002US-00112193.
XX
PR 23-SEP-1996; 96US-0026943P.
XX 11-SEP-1997; 97US-00928069.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI: 2003-438872/41.
DR N-PSDB; ACA61691.
XX
XX New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.
XX
PS Claim 5; Fig 8; 50pp; English.
XX
CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-3
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

| | | | |
|-----------|-----|---|--|
| QY | 61 | CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG | 120 |
| Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG | 120 |
| QY | 121 | WFVECVQSVCSPPFYCQPCDCLDGCALHRRHRLLCSSRDTCGTCPLPGFYEHDGCVSCP | 180 |
| Db | 121 | WFVECVQSVCSPPFYCQPCDCLDGCALHRRHRLLCSSRDTCGTCPLPGFYEHDGCVSCP | 180 |
| QY | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVWLLIGATLTYTTRHCWPHKPLVTADDEAG | 240 |
| Db | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVWLLIGATLTYTTRHCWPHKPLVTADDEAG | 240 |
| QY | 241 | MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTGCPYETQALCPQVTWSW | 300 |
| Db | 241 | MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTGCPYETQALCPQVTWSW | 300 |
| QY | 301 | DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE | 360 |
| Db | 301 | DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE | 360 |
| QY | 361 | IEAVEVEIGFRDQOQYEMLRKRWQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP | 417 |
| Db | 361 | IEAVEVEIGFRDQOQYEMLRKRWQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP | 417 |
| RESULT 14 | | | |
| ADA00738 | | | |
| XX | ID | ADA00738 standard; protein; 417 AA. | |
| AC | AC | ADA00738; | |
| XX | DT | 06-NOV-2003 (first entry) | |
| XX | DE | Human GENCEPTIN protein SEQ ID NO:2. | |
| XX | KW | GENCEPTIN; obesity; lipid partitioning; lipid metabolism; | |
| KW | KW | insulin-like activity; free fatty acid oxidation; weight reduction; | |
| KW | KW | anorectic; antilipemic; antiarteriosclerotic; cardiant; antidiabetic; | |
| KW | KW | hypotensive; ophthalmological; neuroprotective; nephrotropic; | |
| KW | KW | obesity-related disease; insulin resistance; atherosclerosis; | |
| KW | KW | atheromatous disease; heart disease; cardiac insufficiency; | |
| KW | KW | coronary insufficiency; high blood pressure; hypertension; stroke; | |
| KW | KW | syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia; | |
| KW | KW | diabetic complication; microangiopathic lesion; ocular lesion; | |
| KW | KW | retinopathy; neuropathy; renal lesion. | |
| XX | OS | Homo sapiens. | |
| XX | FH | Key | Location/Qualifiers |
| FT | FT | Peptide | 1..24 |
| FT | FT | Protein | /label= signal |
| FT | FT | Domain | 25..417 |
| FT | FT | Region | /label= GENCEPTIN |
| FT | FT | Region | 25..199 |
| FT | FT | Region | /label= EC_domain |
| FT | FT | Region | 34..71 |
| FT | FT | Region | /note= "Cys rich region" |
| FT | FT | Region | 72..115 |
| FT | FT | Region | /note= "Cys rich region" |
| FT | FT | Misc-difference | 97 |
| FT | FT | Misc-difference | 98 |
| FT | FT | Misc-difference | 99 |
| FT | FT | Region | /note= "polymorphic amino acid Glu or Asp" |
| FT | FT | Region | /note= "polymorphic amino acid Gln or Glu" |
| FT | FT | Region | 116..163 |
| FT | FT | Region | /note= "Cys rich region" |
| FT | FT | Region | 164..192 |
| FT | FT | Region | /note= "Cys rich region" |
| FT | FT | Misc-difference | 167 |
| FT | FT | Misc-difference | 168 |
| FT | FT | Domain | /note= "polymorphic amino acid Pro or Leu" |
| FT | FT | Domain | 200..222 |
| FT | FT | Domain | /label= transmembrane_domain |
| FT | FT | Domain | 223..417 |

| | | | | |
|-----------------|-----|---|---------------------------------------|--|
| FT | | /label = IC_domain | | |
| Misc-difference | 312 | | | |
| FT | | /note= "polymorphic amino acid Ala or Arg" | | |
| Misc-difference | 370 | | | |
| FT | | /note= "polymorphic amino acid Arg or Leu" | | |
| Misc-difference | 381 | | | |
| FT | | /note= "polymorphic amino acid Arg or His" | | |
| XX | | | | |
| PN | | W02003013581-A1. | | |
| XX | | | | |
| PD | | 20-FEB-2003. | | |
| XX | | | | |
| PF | | 31-JUL-2002; 2002WO-1B003418. | | |
| XX | | | | |
| PR | | 03-AUG-2001; 2001US-0309818P. | | |
| XX | | | | |
| XX | | (GEST) GENSET SA. | | |
| PA | | | | |
| XX | | Lucas J, Dialynas D, Briggs K; | | |
| PI | | | | |
| XX | | WPI; 2003-268159/26. | | |
| DR | | N-PSDB; ADA00737. | | |
| DR | | | | |
| XX | | | | |
| PT | | New use of Genceptin agonists or antagonists for treating or preventing | | |
| PT | | obesity-related diseases or disorders. | | |
| XX | | | | |
| PS | | Disclosure; Page 33-34; 37pp; English. | | |
| XX | | | | |
| CC | | The present invention describes the use of an agonist or antagonist of | | |
| CC | | GENCEPTIN activity for preventing or treating obesity. Also described is | | |
| CC | | a method of screening for GENCEPTIN activity such as lipid partitioning, | | |
| CC | | lipid metabolism, insulin-like activity, free fatty acid oxidation, and | | |
| CC | | weight reduction. GENCEPTIN has anorectic, antilipemic, | | |
| CC | | antiarteriosclerotic, cardiant, antidiabetic, hypotensive, | | |
| CC | | ophthalmological, neuroprotective and nephrotropic activities. GENCEPTIN | | |
| CC | | can be used for treating or preventing obesity-related diseases or | | |
| CC | | disorders, e.g. obesity, insulin resistance, atherosclerosis, | | |
| CC | | atheromatous disease, heart disease (e.g. cardiac insufficiency, coronary | | |
| CC | | insufficiency, high blood pressure), hypertension, stroke, syndrome X, | | |
| CC | | diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, | | |
| CC | | also diabetic complications, e.g. microangiopathic lesions, ocular | | |
| CC | | lesions, retinopathy, neuropathy and renal lesions. The present sequence | | |
| CC | | represents human GENCEPTIN, which is given in the exemplification of the | | |
| CC | | present invention. | | |
| XX | | | | |
| SQ | | Sequence 417 AA; | | |
| | | Query Match | 100.0%; Score 2323; DB 6; Length 417; | |
| | | Best Local Similarity | 100.0%; Pred. No. 1.5e-161; | |
| | | Matches 417; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 1 | MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCPCPAGHYLKAP | 60 | |
| Db | 1 | MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCPCPAGHYLKAP | 60 | |
| Qy | 61 | CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG | 120 | |
| Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG | 120 | |
| Qy | 121 | WFVECVQSVCSPPFYCQPCDCLDGCALHRRHRLTLLCSSRDTCGTCPLPGFYEHDGCVSCP | 180 | |
| Db | 121 | WFVECVQSVCSPPFYCQPCDCLDGCALHRRHRLTLLCSSRDTCGTCPLPGFYEHDGCVSCP | 180 | |
| Qy | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVWPLLLGATLTYTTRHCWPHKPLVTADDEAG | 240 | |
| Db | 181 | TSTLGSCPERCAAVCGWRQFWQVLLAGLVWPLLLGATLTYTTRHCWPHKPLVTADDEAG | 240 | |
| Qy | 241 | MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTGCPYETQALCPQVTWSW | 300 | |
| Db | 241 | MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTGCPYETQALCPQVTWSW | 300 | |
| Qy | 301 | DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE | 360 | |

Db 301 DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
 QY 361 IEAVEVEIGRFRDQOQYEMLKRWKQQQAGLGVYAALERMGLDGCVEDLSRLQGP 417
 |||||||
 Db 361 IEAVEVEIGRFRDQOQYEMLKRWKQQQAGLGVYAALERMGLDGCVEDLSRLQGP 417
 RESULT 15
 ABG73824
 ID ABG73824 standard; protein; 417 AA.
 XX
 AC ABG73824;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE Human apoptotic protein, Apo-3.
 XX
 KW human; Apo-2 ligand inhibitor; Apo-2LI; apoptosis; NF-kappaB; JNK;
 KW c-Jun N-terminal kinase; necrosis factor kappa B; chimeric molecule;
 KW tissue-specific typing; Apo-3; transgenic; affinity purification;
 KW competitive-type receptor binding assay.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..198
 FT /label= Extracellular_domain
 FT Protein 1..181
 FT /label= Apo-2LI
 FT /note= "Specifically claimed in claim 4. Residues 1-181
 FT of Apo-3 represent Apo2LI"
 FT 34..71
 FT /label= Cysteine-rich_domain_1
 FT 72..115
 FT /label= Cysteine-rich_domain_2
 FT 116..163
 FT /label= Cysteine-rich_domain_3
 FT 164..181
 FT /label= Cysteine-rich_domain_4
 FT /note= "This cysteine-rich domain is apparently truncated
 FT in Apo-2LI and contains only 3 cysteines instead of 6."
 FT 338..417
 FT /label= Death_domain
 XX
 US2002146768-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 19-NOV-2001; 2001US-00993234.
 XX
 PR 01-APR-1996; 96US-00625328.
 PR 23-SEP-1996; 96US-00710802.
 PR 31-MAR-1997; 97US-00828683.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ;
 XX
 DR WPI; 2003-174176/17.
 DR N-PSDB; ABX15507, ABX15003.
 XX
 PT New isolated biologically active Apo-2LI or Apo-3 used to induce
 PT apoptosis in mammalian cells.
 XX
 PS Claim 22; Fig 4; 44pp; English.
 XX
 CC The invention relates to an isolated biologically active Apo-2LI or Apo-3
 CC which has at least 80% sequence identity with native sequence Apo-2LI
 CC having 1-181 amino acids or Apo-3 having 1-417 amino acids, respectively.
 CC Apo-3 can be employed therapeutically to induce apoptosis or NF-kappaB or
 CC JNK mediated gene expression in mammalian cells. The Apo-3 chimeric
 CC molecules can be employed therapeutically to inhibit apoptosis; necrosis
 CC factor (NF)-kappaB induction; c-Jun N-terminal kinase (JNK) activation.

CC Apo-2LI can be employed therapeutically to inhibit mammalian cell
 CC apoptosis in vivo or ex vivo. Nucleic acid sequences encoding the Apo-3
 CC or Apo-2LI may be used as a diagnostic for tissue-specific typing. The
 CC isolated Apo-3 or Apo-2LI may be used in quantitative diagnostic assays
 CC as a control against which samples containing unknown quantities of Apo-3
 CC or Apo-2LI may be prepared. Apo-3 preparations are also useful in
 CC generating antibodies, as standards in assays for Apo-3 or Apo-2LI, in
 CC affinity purification techniques, and in competitive-type receptor
 CC binding assays when labelled with, e.g. radioiodine, enzymes, or
 CC fluorophores. Modified forms of the Apo-3, e.g. Apo-3-IgG chimeric
 CC molecules can be used as immunogens in producing anti-Apo-3 antibodies.
 CC Nucleic acids which encode Apo-3 or its modified forms can also be used
 CC to generate either transgenic animals or knock out animals, e.g. mouse or
 CC rat, which, in turn, are useful in the development and screening of
 CC therapeutically useful reagents. The Apo-3 polypeptide stimulates or
 CC induces apoptotic activity in mammalian cells. The present sequence
 CC represents the human apoptotic protein, Apo-3. Residues 1-181 of Apo3
 CC represent Apo2LI which may be a secreted or soluble form of Apo3
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.5e-161;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 |||||||
 Db 1 MEQPRGCAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSAVADTRCGCKPG 120
 |||||||
 Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCSAVADTRCGCKPG 120
 QY 121 WFVECOVSCVSSSPYFCPLDCGALHRRHRLTLLCSRRDTCCTCLPGFYEHGDCVSCP 180
 |||||||
 Db 121 WFVECOVSCVSSSPYFCPLDCGALHRRHRLTLLCSRRDTCCTCLPGFYEHGDCVSCP 180
 QY 181 TSTLGSCPERCAAVCGMRQMFVQVLLAGLVPLLLGATLTYYRHCHWPKPLVTADAG 240
 |||||||
 Db 181 TSTLGSCPERCAAVCGMRQMFVQVLLAGLVPLLLGATLTYYRHCHWPKPLVTADAG 240
 QY 241 MEALTPPPATHLSPLDSAHTLAPDSSEKICTVQLVGNHSWTGYPETQALCPQVTWSW 300
 |||||||
 Db 241 MEALTPPPATHLSPLDSAHTLAPDSSEKICTVQLVGNHSWTGYPETQALCPQVTWSW 300
 QY 301 DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
 |||||||
 Db 301 DQLPSRALGPAAATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
 QY 361 IEAVEVEIGRFRDQOQYEMLKRWKQQQAGLGVYAALERMGLDGCVEDLSRLQGP 417
 |||||||
 Db 361 IEAVEVEIGRFRDQOQYEMLKRWKQQQAGLGVYAALERMGLDGCVEDLSRLQGP 417

Search completed: March 20, 2006, 08:00:42
 Job time : 88 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:00:54 ; Search time 72 Seconds
(without alignments)
2419.928 Million cell updates/sec

Title: US-10-081-280-6
Perfect score: 2323
Sequence: 1 MEQPRGCAAAVALLVLL.....ERMGLDGCVEDLRLRQRP 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pgp:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pgp:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pgp:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 2323 | 100.0 | 417 | 3 | US-09-333-966-4 |
| 2 | 2323 | 100.0 | 417 | 3 | US-09-874-138-5 |
| 3 | 2323 | 100.0 | 417 | 3 | US-09-993-234-6 |
| 4 | 2323 | 100.0 | 417 | 3 | US-09-314-889-4 |
| 5 | 2323 | 100.0 | 417 | 4 | US-10-005-842-5 |
| 6 | 2323 | 100.0 | 417 | 4 | US-10-081-280-6 |
| 7 | 2323 | 100.0 | 417 | 4 | US-10-112-793-6 |
| 8 | 2323 | 100.0 | 417 | 4 | US-10-112-193-10 |
| 9 | 2323 | 100.0 | 417 | 4 | US-10-175-902-5 |
| 10 | 2323 | 100.0 | 417 | 4 | US-10-189-189-4 |
| 11 | 2323 | 100.0 | 417 | 4 | US-10-210-951-24 |
| 12 | 2323 | 100.0 | 417 | 4 | US-10-211-884-24 |
| 13 | 2323 | 100.0 | 417 | 4 | US-10-310-793-4 |
| 14 | 2323 | 100.0 | 417 | 4 | US-10-311-858-24 |
| 15 | 2323 | 100.0 | 417 | 4 | US-10-415-247-3 |
| 16 | 2323 | 100.0 | 417 | 4 | US-10-648-825-5 |
| 17 | 2323 | 100.0 | 417 | 4 | US-10-774-622-5 |
| 18 | 2323 | 100.0 | 417 | 4 | US-10-744-379-2 |
| 19 | 2323 | 100.0 | 417 | 5 | US-10-979-831-5 |
| 20 | 2323 | 100.0 | 833 | 4 | US-10-226-296-5 |
| 21 | 2323 | 100.0 | 833 | 4 | US-10-226-318-5 |
| 22 | 2323 | 100.0 | 833 | 4 | US-10-648-786-5 |
| 23 | 2323 | 100.0 | 833 | 5 | US-10-648-786-5 |
| 24 | 2267 | 97.6 | 428 | 3 | US-09-333-966-2 |
| 25 | 2267 | 97.6 | 428 | 3 | US-09-314-889-2 |
| 26 | 2267 | 97.6 | 428 | 4 | US-10-189-189-2 |
| 27 | 1404 | 60.4 | 411 | 4 | US-10-744-379-6 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 1051 | 45.2 | 181 | 3 | US-09-884-733-1 | Sequence 1, Appli |
| 29 | 1051 | 45.2 | 181 | 3 | US-09-993-234-1 | Sequence 1, Appli |
| 30 | 1051 | 45.2 | 181 | 4 | US-10-081-280-1 | Sequence 1, Appli |
| 31 | 1051 | 45.2 | 181 | 4 | US-10-112-793-1 | Sequence 1, Appli |
| 32 | 1051 | 45.2 | 181 | 4 | US-10-112-193-1 | Sequence 1, Appli |
| 33 | 1051 | 45.2 | 188 | 4 | US-10-415-247-5 | Sequence 5, Appli |
| 34 | 404.5 | 17.4 | 454 | 4 | US-10-410-012-3 | Sequence 3, Appli |
| 35 | 404.5 | 17.4 | 454 | 4 | US-10-799-345-24 | Sequence 24, Appli |
| 36 | 394.5 | 17.0 | 461 | 4 | US-10-748-112-21 | Sequence 21, Appli |
| 37 | 387.5 | 16.7 | 471 | 3 | US-09-970-532-2 | Sequence 2, Appli |
| 38 | 381 | 16.4 | 74 | 3 | US-09-887-879-15 | Sequence 15, Appli |
| 39 | 381 | 16.4 | 74 | 3 | US-09-992-964-15 | Sequence 15, Appli |
| 40 | 381 | 16.4 | 74 | 4 | US-10-207-295-9 | Sequence 9, Appli |
| 41 | 381 | 16.4 | 74 | 4 | US-10-242-383-15 | Sequence 15, Appli |
| 42 | 380.5 | 16.4 | 461 | 3 | US-09-899-422-15 | Sequence 15, Appli |
| 43 | 380.5 | 16.4 | 461 | 3 | US-09-898-234-15 | Sequence 15, Appli |
| 44 | 380.5 | 16.4 | 461 | 3 | US-09-899-429A-25 | Sequence 25, Appli |
| 45 | 380.5 | 16.4 | 461 | 3 | US-09-792-356-15 | Sequence 15, Appli |

ALIGNMENTS

RESULT 1
US-09-333-966-4
; Sequence 4, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-333-966-4

Query Match
Best Local Similarity 100.0%; Score 2323; DB 3; Length 417;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENC SAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENC SAVADTRCGCKPG 120

Qy 121 WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTC LFGFYEHDGCVSCP 180
Db 121 WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTC LFGFYEHDGCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTTRH CWPBKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTTRH CWPBKPLVTAD EAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSSEKICTVQLVGN S WTPGYPETOEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSSEKICTVQLVGN S WTPGYPETOEALCPQVTWSW 300

Qy 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFRDQOQYEMLRKWRQQQPGAGLVAYAA LERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLRKWRQQQPGAGLVAYAA LERMGLDGCVEDLRSRLQRP 417

RESULT 3
US-09-993-234-6
; Sequence 6, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 19-NO. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match
Best Local Similarity 100.0%; Score 2323; DB 3; Length 417;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60

Qy 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENC SAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENC SAVADTRCGCKPG 120

Qy 121 WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTC LFGFYEHDGCVSCP 180
Db 121 WFVECVQSVQCVSSSPFYCQCLDCGALHRRHRLLCRRDDTCGTC LFGFYEHDGCVSCP 180

Qy 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTTRH CWPBKPLVTAD EAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTTRH CWPBKPLVTAD EAG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSSEKICTVQLVGN S WTPGYPETOEALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSSEKICTVQLVGN S WTPGYPETOEALCPQVTWSW 300

Qy 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLREAE 360

Qy 361 IEAVEVEIGRFRDQOQYEMLRKWRQQQPGAGLVAYAA LERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLRKWRQQQPGAGLVAYAA LERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-09-874-138-5
; Sequence 5, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.131006
; CURRENT APPLICATION NUMBER: US/09/874,138
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-5

Query Match
Best Local Similarity 100.0%; Score 2323; DB 3; Length 417;
```

US-09-993-234-6

Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCNSAVADTRCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCNSAVADTRCCKPG 120

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180

QY 181 TSTLGSCEPCAAVAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCEPCAAVAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240

QY 241 MEALTPPPATHLSPLDSAHTLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHTLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDVAVPARWKKEFVRTLGLREAE 360
DB 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDVAVPARWKKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYQYEMLKRWRQOQAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYQYEMLKRWRQOQAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 4

US-09-314-889-4
; Sequence 4, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/815,469
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-314-889-4

Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAAAVALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCNSAVADTRCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCNSAVADTRCCKPG 120

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180

QY 181 TSTLGSCEPCAAVAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCEPCAAVAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTADAEAG 240

QY 241 MEALTPPPATHLSPLDSAHTLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHTLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDVAVPARWKKEFVRTLGLREAE 360
DB 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDVAVPARWKKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYQYEMLKRWRQOQAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYQYEMLKRWRQOQAGLVAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 5

US-10-005-842-5
; Sequence 5, Application US/10005842
; Publication No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Gentz, Reiner
; Yu, Guo-Liang
; Su, Jeffrey
; Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/005,842

```

; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,583
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/040,846
; FILING DATE: 17-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF366
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3013098504
; TELEFAX: 3013098439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-005-842-5

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
QY 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTAD EAG 240
DB 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTAD EAG 240
QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQQYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQQYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 6
US-10-081-280-6
; Sequence 6, Application US/10081280
; Publication No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: F1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-081-280-6

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
QY 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTAD EAG 240
DB 181 TSTLGSQPCERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTAD EAG 240
QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQQYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQQYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 7
US-10-112-793-6
; Sequence 6, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

```


COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/112,793
 FILING DATE: 28-Mar-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/828,693A
 FILING DATE: 31-Mar-1997
 APPLICATION NUMBER: 08/623328
 FILING DATE: 1-Apr-1996
 APPLICATION NUMBER: 08/110802
 FILING DATE: 23-Sep-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1007P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 417 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-112-793-6

Query Match 100.0%; Score 2323; DB 4; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 DB 1 MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
 DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
 QY 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
 DB 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
 QY 181 TSTLGSCEPCRCACVCGWRQMFVQVLLAGLVVPLLGGATLTYTRHCWPHKPLVTADG 240
 DB 181 TSTLGSCEPCRCACVCGWRQMFVQVLLAGLVVPLLGGATLTYTRHCWPHKPLVTADG 240
 QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 DB 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 QY 301 DQLPSALGPAAPATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 DB 301 DQLPSALGPAAPATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 QY 361 IEAVEVEIGRFDDQYEMLKRWQQQPAGIGAVYAALERMGLDGCVEDLRSRLQRP 417
 DB 361 IEAVEVEIGRFDDQYEMLKRWQQQPAGIGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 8
 US-10-112-193-10
 ; Sequence 10, Application US/10112193
 ; Publication No. US20030004313A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/112,193
 FILING DATE: 28-Mar-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/928,069
 FILING DATE: 11-Sep-1997
 APPLICATION NUMBER: 60/026943
 FILING DATE: 23-Sep-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1052R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 417 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-112-193-10

Query Match 100.0%; Score 2323; DB 4; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 DB 1 MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
 DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
 QY 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
 DB 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
 QY 181 TSTLGSCEPCRCACVCGWRQMFVQVLLAGLVVPLLGGATLTYTRHCWPHKPLVTADG 240
 DB 181 TSTLGSCEPCRCACVCGWRQMFVQVLLAGLVVPLLGGATLTYTRHCWPHKPLVTADG 240
 QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 DB 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 QY 301 DQLPSALGPAAPATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 DB 301 DQLPSALGPAAPATLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 QY 361 IEAVEVEIGRFDDQYEMLKRWQQQPAGIGAVYAALERMGLDGCVEDLRSRLQRP 417
 DB 361 IEAVEVEIGRFDDQYEMLKRWQQQPAGIGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 9
 US-10-175-902-5
 ; Sequence 5, Application US/10175902

Publication No. US20030108516A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Roben, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.130005
; CURRENT APPLICATION NUMBER: US/10/175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5,7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP | 60 |
| DB | 1 | MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP | 60 |
| QY | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| DB | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| QY | 121 | WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP | 180 |
| DB | 121 | WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP | 180 |
| QY | 181 | TSTLGSCPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTAD | 240 |
| DB | 181 | TSTLGSCPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTAD | 240 |
| QY | 241 | MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| DB | 241 | MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| QY | 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKKEFVRTLGLEAE | 360 |
| DB | 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKKEFVRTLGLEAE | 360 |
| QY | 361 | IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP | 417 |
| DB | 361 | IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP | 417 |

RESULT 10
US-10-189-189-4
; Sequence 4, Application US/10189189
; Publication No. US20030170203A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors

FILE REFERENCE: 1488.031000C
; CURRENT APPLICATION NUMBER: US/10/189,189
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/314,314
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/303,155
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 09/557,908
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-189-4

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5,7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP | 60 |
| DB | 1 | MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP | 60 |
| QY | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| DB | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| QY | 121 | WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP | 180 |
| DB | 121 | WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP | 180 |
| QY | 181 | TSTLGSCPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTAD | 240 |
| DB | 181 | TSTLGSCPCERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTAD | 240 |
| QY | 241 | MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| DB | 241 | MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| QY | 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKKEFVRTLGLEAE | 360 |
| DB | 301 | DQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKKEFVRTLGLEAE | 360 |
| QY | 361 | IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP | 417 |
| DB | 361 | IEAVEVEIGRFRDQOQYEMLKRWQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP | 417 |

RESULT 11
US-10-210-951-24
; Sequence 24, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/210,951
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 24
LENGTH: 417
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-951-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSCVSSPPFYCQPCDCLGALHRRHRLLCRRDDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSCVSSPPFYCQPCDCLGALHRRHRLLCRRDDTCGTCLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCTPCERCAACVGRQMFVQVLLAGLVVPLLIGATLITYYRHCHWPKPLVTADAEAG 240
Db 181 TSTLGSCTPCERCAACVGRQMFVQVLLAGLVVPLLIGATLITYYRHCHWPKPLVTADAEAG 240

Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300

Qy 301 DOLPSRALGPAAPATLSPSPAGSPAMLOPGPOLYDMDAVPARRWKEFVRLTGLREAE 360
Db 301 DOLPSRALGPAAPATLSPSPAGSPAMLOPGPOLYDMDAVPARRWKEFVRLTGLREAE 360

Qy 361 IEAVEVEIGFRDQOQYEMLXKRWQOQAGLVAVVAALERMGLDGCVEDLSRLQRP 417
Db 361 IEAVEVEIGFRDQOQYEMLXKRWQOQAGLVAVVAALERMGLDGCVEDLSRLQRP 417

US-10-211-884-24
Sequence 24, Application US/10211884
Publication No. US20030175900A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 24
LENGTH: 417
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-884-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSCVSSPPFYCQPCDCLGALHRRHRLLCRRDDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECVQSCVSSPPFYCQPCDCLGALHRRHRLLCRRDDTCGTCLPGFYEHGDCVSCP 180

Qy 181 TSTLGSCTPCERCAACVGRQMFVQVLLAGLVVPLLIGATLITYYRHCHWPKPLVTADAEAG 240
Db 181 TSTLGSCTPCERCAACVGRQMFVQVLLAGLVVPLLIGATLITYYRHCHWPKPLVTADAEAG 240

Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300

Qy 301 DQPSRAGPAAAPTLSPEPAGSPAMWLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQPSRAGPAAAPTLSPEPAGSPAMWLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEIGRFRDQOYEMLRKRWQOOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417
Db 361 IEAVEIGRFRDQOYEMLRKRWQOOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417

RESULT 13
US-10-310-793-4
; Sequence 4, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: P5573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: human
US-10-310-793-4

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARQCAQDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARQCAQDEQASQVALENCNSAVADTRCGCKPG 120
Qy 121 WFVEQCVSQVSSPFFCQCLDCGALHRTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
Db 121 WFVEQCVSQVSSPFFCQCLDCGALHRTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSCPERCAAVCGWRQFWQVLLAGVWPLLGLATLTYTYRHCWPKPLVTADG 240
Db 181 TSTLGSCPERCAAVCGWRQFWQVLLAGVWPLLGLATLTYTYRHCWPKPLVTADG 240

Qy 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300
Qy 301 DQPSRAGPAAAPTLSPEPAGSPAMWLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQPSRAGPAAAPTLSPEPAGSPAMWLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEIGRFRDQOYEMLRKRWQOOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417
Db 361 IEAVEIGRFRDQOYEMLRKRWQOOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417

RESULT 14

US-10-211-858-24
; Sequence 24, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 24
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARQCAQDEQASQVALENCNSAVADTRCGCKPG 120

| | | | |
|----|-----|---|-----|
| Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| QY | 121 | WFVECVQSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP | 180 |
| Db | 121 | WFVECVQSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP | 180 |
| QY | 181 | TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWPHKPLVTAD | 240 |
| Db | 181 | TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWPHKPLVTAD | 240 |
| QY | 241 | MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| Db | 241 | MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| QY | 301 | DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| Db | 301 | DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE | 360 |
| QY | 361 | IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP | 417 |
| Db | 361 | IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP | 417 |

Search completed: March 20, 2006, 08:02:18
Job time : 74 secs

RESULT 15
US-10-415-247-3
; Sequence 3, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOPI-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-3

| | | | |
|--|-----|---|-----|
| Query Match 100.0%; Score 2323; DB 4; Length 417; Best Local Similarity 100.0%; Pred. No. 5.7e-163; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 | MEORPRGCAVAAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP | 60 |
| Db | 1 | MEORPRGCAVAAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP | 60 |
| QY | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| Db | 61 | CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG | 120 |
| QY | 121 | WFVECVQSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP | 180 |
| Db | 121 | WFVECVQSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP | 180 |
| QY | 181 | TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWPHKPLVTAD | 240 |
| Db | 181 | TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWPHKPLVTAD | 240 |
| QY | 241 | MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |
| Db | 241 | MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW | 300 |

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7.
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:00:54 ; Search time 29 Seconds
(without alignments)
411.577 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLVLL.....ERMGLDGCVEDLRSLRQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 2862289 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pdb.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2323 | 100.0 | 417 | 7 | US-11-174-467-10 |
| 2 | 2323 | 100.0 | 418 | 6 | US-10-512-325-3 |
| 3 | 2323 | 100.0 | 418 | 7 | US-11-196-919-2 |
| 4 | 2323 | 100.0 | 833 | 7 | US-11-076-187-5 |
| 5 | 1051 | 45.2 | 181 | 7 | US-11-174-467-1 |
| 6 | 381 | 16.4 | 74 | 7 | US-11-116-746-15 |
| 7 | 374.5 | 16.1 | 909 | 7 | US-11-076-187-4 |
| 8 | 374 | 16.1 | 455 | 7 | US-11-182-946-3 |
| 9 | 364.5 | 15.7 | 453 | 7 | US-11-185-878-5 |
| 10 | 206.5 | 8.9 | 283 | 6 | US-10-987-663-4 |
| 11 | 200.5 | 8.6 | 161 | 7 | US-11-126-126-2 |
| 12 | 200.5 | 8.6 | 161 | 7 | US-11-057-923-3 |
| 13 | 199.5 | 8.6 | 335 | 7 | US-11-182-946-7 |
| 14 | 199.5 | 8.6 | 669 | 7 | US-11-076-187-3 |
| 15 | 197 | 8.5 | 331 | 7 | US-11-185-878-3 |
| 16 | 192 | 8.3 | 32 | 7 | US-11-196-919-4 |
| 17 | 191 | 8.2 | 411 | 7 | US-11-116-746-11 |
| 18 | 191 | 8.2 | 411 | 7 | US-11-245-053-1 |
| 19 | 190 | 8.2 | 32 | 6 | US-10-512-325-5 |
| 20 | 172 | 7.4 | 1198 | 6 | US-10-453-372-880 |
| 21 | 171.5 | 7.4 | 934 | 6 | US-10-453-372-1158 |
| 22 | 166 | 7.1 | 435 | 7 | US-11-077-386-19 |
| 23 | 166 | 7.1 | 450 | 7 | US-11-077-386-20 |
| 24 | 166 | 7.1 | 3597 | 7 | US-11-019-711-6 |
| 25 | 166 | 7.1 | 3600 | 7 | US-11-019-711-2 |

26 164 7.1 399 7 US-11-077-386-18 Sequence 18, Appl
27 163.5 7.0 355 7 US-11-182-946-14 Sequence 14, Appl
28 163.5 7.0 415 7 US-11-182-946-6 Sequence 6, Appl
29 162.5 7.0 334 6 US-10-514-057-6 Sequence 6, Appl
30 162.5 7.0 349 7 US-11-182-946-13 Sequence 13, Appl
31 162.5 7.0 467 7 US-11-185-878-6 Sequence 6, Appl
32 162 7.0 612 6 US-10-453-372-1156 Sequence 1156, Ap
33 161 6.9 418 7 US-11-116-746-14 Sequence 14, Appl
34 161 6.9 468 7 US-11-076-187-2 Sequence 2, Appl
35 160 6.9 468 6 US-10-995-561-907 Sequence 907, App
36 159.5 6.9 350 7 US-11-132-285-41 Sequence 41, Appl
37 159 6.8 229 6 US-10-924-074-8 Sequence 8, Appl
38 159 6.8 237 6 US-10-924-074-6 Sequence 6, Appl
39 158 6.8 1574 6 US-10-055-877-211 Sequence 211, App
40 157 6.8 3690 6 US-10-995-561-1016 Sequence 1016, Ap
41 155.5 6.7 427 7 US-11-182-946-5 Sequence 5, Appl
42 155.5 6.7 427 7 US-11-185-878-4 Sequence 4, Appl
43 155 6.7 78 7 US-11-116-746-16 Sequence 16, Appl
44 155 6.7 3717 6 US-10-821-234-1076 Sequence 1076, Ap
45 152 6.5 3714 6 US-10-995-561-1015 Sequence 1015, Ap

ALIGNMENTS

RESULT 1

US-11-174-467-10
; Sequence 10, Application US/11/174467
; Publication No. US20060041106A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/174,467
; FILING DATE: 06-Jul-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-11-174-467-10

Query Match 100.0%; Score 2323; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Qy 181 TSTLGSPCRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADDEAG 240
Db 181 TSTLGSPCRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTWSW 300
Qy 301 DQLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLRWQOQOQAGLVAVYALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFRDQOQYEMLRWQOQOQAGLVAVYALERMGLDGCVEDLRSRLQGP 417
```

RESULT 2

```
US-10-512-325-3
; Sequence 3, Application US/10512325
; Publication No. US20060013822A1
; GENERAL INFORMATION:
; APPLICANT: Tittle, Thomas V.
; APPLICANT: Wegmann, Keith W.
; TITLE OF INVENTION: UTILIZATION OF MHC CLASS II BINDING
; TITLE OF INVENTION: MOTIFS IN IMMUNIZATION TO PRODUCE IMMUNE SERUM, MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND VACCINES
; FILE REFERENCE: TW 2003.00
; CURRENT APPLICATION NUMBER: US/10/512,325
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: 60/367,042
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US03/08963
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (14)...(32)
; OTHER INFORMATION: Extended peptide shown to be the B cell epitope
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(13)
; OTHER INFORMATION: Peptide fragment
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(32)
; OTHER INFORMATION: Peptide fragment
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (14)...(32)
; OTHER INFORMATION: Peptide fragment
US-10-512-325-3
```

```
Query Match 100.0%; Score 2323; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Qy 181 TSTLGSPCRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADDEAG 240
Db 181 TSTLGSPCRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTWSW 300
Qy 301 DQLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLRWQOQOQAGLVAVYALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGRFRDQOQYEMLRWQOQOQAGLVAVYALERMGLDGCVEDLRSRLQGP 417
```

RESULT 3

```
US-11-196-919-2
; Sequence 2, Application US/11196919
; Publication No. US2005028223A1
; GENERAL INFORMATION:
; APPLICANT: Tittle, Thomas V.
; APPLICANT: Wegmann, Keith W.
; TITLE OF INVENTION: TR3-SPECIFIC BINDING AGENT AND METHODS
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: TW2001.01
; CURRENT APPLICATION NUMBER: US/11/196,919
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: PCT/US00/31692
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,583
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 10/204,419
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-196-919-2
```

```
Query Match 100.0%; Score 2323; DB 7; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRRTDCGTCCLPGFVHGDCVSCP 180
Qy 181 TSTLGSPCRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADDEAG 240
```


181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTTRHCWPHKPLVTTADEAG 240
241 MEALTTPPPATHLSPDLSAHTLAPDSSSEKICTVQLVGNSTWPGYPTQALCPQVTTWSW 300
241 MEALTTPPPATHLSPDLSAHTLAPDSSSEKICTVQLVGNSTWPGYPTQALCPQVTTWSW 300
301 DQPSRALGPAAPTLLSPSPAGSPAMMLQPGPQLYDVMDDAVPARRWKEFVRTLGLREAE 360
301 DQPSRALGPAAPTLLSPSPAGSPAMMLQPGPQLYDVMDDAVPARRWKEFVRTLGLREAE 360
361 IEAVEVEIGRFRDQOYEMLKRWQOQPGAGLGVAYAAALERMGLDGCVEDLRSRLQRP 417
361 IEAVEVEIGRFRDQOYEMLKRWQOQPGAGLGVAYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 4

US-11-076-187-5
; Sequence 5, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: P335P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-5

Query Match 100.0%; Score 2323; DB 7; Length 833;
Best Local Similarity 100.0%; Pred. No. 4.5e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVECVQSVCSPPFYCQCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVECVQSVCSPPFYCQCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180

QY 181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTTRHCWPHKPLVTTADEAG 240
DB 181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTTRHCWPHKPLVTTADEAG 240
QY 241 MEALTTPPPATHLSPDLSAHTLAPDSSSEKICTVQLVGNSTWPGYPTQALCPQVTTWSW 300
DB 241 MEALTTPPPATHLSPDLSAHTLAPDSSSEKICTVQLVGNSTWPGYPTQALCPQVTTWSW 300
QY 301 DQPSRALGPAAPTLLSPSPAGSPAMMLQPGPQLYDVMDDAVPARRWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAPTLLSPSPAGSPAMMLQPGPQLYDVMDDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOYEMLKRWQOQPGAGLGVAYAAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOYEMLKRWQOQPGAGLGVAYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 5

US-11-174-467-1
; Sequence 1, Application US/11174467
; Publication No. US20060041106A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/174,467
; FILING DATE: 06-Jul-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-11-174-467-1

Query Match 45.2%; Score 1051; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 8.5e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120

QY 121 WFEVCQVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFEVCQVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180

QY 181 T 181
Db 181 T 181

RESULT 6

US-11-116-746-15
; Sequence 15, Application US/11116746
; Publication No. US20060020114A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2cR
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/11/116,746
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-116-746-15

Query Match 16.4%; Score 381; DB 7; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAAL 397
Db 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOYEMLKRWROQOPAGLGAVYAAL 60

QY 398 ERMGLDGCVEDLRS 411

Db 61 ERMGLDGCVEDLRS 74

RESULT 7

US-11-076-187-4
; Sequence 4, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 4
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-4

Query Match 16.1%; Score 374.5; DB 7; Length 909;

Best Local Similarity 28.5%; Pred. No. 7.6e-22;
Matches 132; Conservative 49; Mismatches 181; Indels 101; Gaps 23;

QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

Db 14 LLELLVGIYPSGVIGLVPHLGDREKDSVCPQCKYIHPQNNSSICCTKCHKGTLYLNDCPG 73

QY 64 PCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGWVF 123

Db 74 P-GDITDCRECESGSFTASENHLR-HCLSCSKCKEMQVEISSCTVDRTVCGCRKNQYR 131

QY 124 EC---QVSQCVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180

Db 132 HYWSENLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 180

QY 181 TSTLGSQCE--RCAAVC-----GWRQMFVQVLLAGLVPLLIGATITTYTRH 226

Db 181 ----SNCKSLECKLCLPQIENVKTEDSGTIVLLPLVIFFGCLLSLLFGLMYRYQR 236

QY 227 CWPBK-----PLVTADKAMEALTPPPATHLSPLDS-----AHTLLAPDSSSKIC 272

Db 237 -WKSPLYIVCGKSTPEKEGELEGTTKP---LAPNPSFSPPTPGFTPTLGFSPVPSSTFT 292

QY 273 TVOLVGNSTWTPGYPETEALCPQVTSWDOLPSRALGP-----AAAPTLS- 318

Db 293 S-----SSTYTPGD-----CPNFA-----APREVAPPYQGDAPILATLASDIPNPL 336

QY 319 ---ESPAGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373

Db 337 QKWEDSAHKPQSLDTPDPAFLYAVENVPLRWKEFVRLGLSDHEIDRLQLONGRCLRE 396

QY 374 QOYEMLKRWROQOP---AGLGAVYAALERNGLDGCVEDLRSRL 413

Db 397 AQYSMLATWRRRTPREATLELIGRVLRDMDLIGCLEIDREAL 439

RESULT 8

US-11-182-946-3
; Sequence 3, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT

ORGANISM: Homo sapiens
US-11-182-946-3

Query Match 16.1%; Score 374; DB 7; Length 455;
Best Local Similarity 28.3%; Pred. No. 3.9e-22;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;

QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
DB 15 LLELLVGIYPSGIVGLPHLGDREKDSVCPQGYIHPQNNISICTCKHGYLYNDPCG 74
QY 64 PCGNTCLVCPQDTFLAWNNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGWVFV 123
DB 75 PQQDTCRECSGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRDTVCGCRKNQYR 133
QY 124 EC---QVSCVSSSPYQPCDCCALHRRHLLCSRRTDCGTCLPGFYEHGDCVSCP 180
DB 134 HYWSNLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182
QY 181 TSTLSCPE--RCAAVC-----GWRQMFVQVLLAGLVVPLLGLATLTYTYRH 226
DB 183 ----SNCKSLECTKLCLOIENVKGTEDSGTTVLLPLVIFGLCLLSLLFGLMYRYOR 238
QY 227 CWPBK-----PLVTADAGMEALTPPPATHLSPLDS-----AHTLLAPDSSEKIC 272
DB 239 -WKSXYLSIVCGKSTPEKEGELETTKP---LAPNPSFSPPTGFTPLGFSVPSSFT 294
QY 273 TVQLVGNSTWPGYPTQALCPQVTSWDLPSRALGP-----AAAPTLS- 318
DB 295 S-----SSTYTPGD-----CPNFA-----APREVAPPYQADPILATALASDPI 338
QY 319 ---ESPAGSPAMMLQPCP-QLYDMDVAPARWKEFVRTLGLREABIEAVEVEIGR-FRD 373
DB 339 QKWESAHKPSQSLDTPATLYAVENVVPLRWKEFVRRLGLSDHEIDRLQNGRCLRE 398
QY 374 QQYEMLKRWROQOP---AGLGAVYAALERMGLDGCVEDLRSRL 413
DB 399 AQYSMLATWRRTPREATLELLGRVLRDMDLLGCLDIEEAL 441

RESULT 9
US-11-185-878-5
; Sequence 5, Application US/11185878
; Publication No. US20050282217A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: PF379P1D1
; CURRENT APPLICATION NUMBER: US/11/185,878
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/280,047
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 453
; TYPE: PRT
; ORGANISM: human

US-11-185-878-5

Query Match 15.7%; Score 364.5; DB 7; Length 453;
Best Local Similarity 28.2%; Pred. No. 2.2e-21;
Matches 126; Conservative 50; Mismatches 178; Indels 93; Gaps 21;

QY 20 LGARAQGTTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPQDTFL 79
DB 33 LGDREKDSVCPQ-----GKYIHPNNSICTCKHGYLYNDPCGQDTCRECSGSFT 88
QY 80 AWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPGWVFEC---QVSCVSSSP 136
DB 89 ASENHLR-HCLSCSKCKEMGQVEISSCTVDRDTVCGCRKNQYRYWSNLFQC-----F 142
QY 137 YCQPCDCCALHRRHLLCSRRTDCGTCLPGFYEHGDCVSCPSTLGSCE--RCAAV 194
DB 143 NCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC-----SNCKSLECTKL 192
QY 195 C-----GWRQMFVQVLLAGLVVPLLGLATLTYTYRHCPHK-----PLVT 235
DB 193 CLPQIENVKGTEDSGTTVLLPLVIFGLCLLSLLFGLMYRYOR-WKSXYLSIVCGKSTP 251
QY 236 ADEAGMEALTPPPATHLSPLDS-----AHTLLAPDSSEKICTVQLVGNSTWTPGYPET 288
DB 252 EKEGELETTKP---LAPNPSFSPPTGFTPLGFSVPSSFTS-----SSTYTPGD--- 301
QY 289 QEALCPQVTSWDLPSRALGP-----AAAPTLS-ESPAGSPAMMLQ 331
DB 302 ----CPNFA-----APREVAPPYQADPILATALASDPIPNLQKWESAHKPSQSLD 352
QY 332 GP-QLYDMDVAPARWKEFVRTLGLREABIEAVEVEIGR-FRDQYEMLKRWROQOP--- 387
DB 353 DPATLYAVENVVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAGYSMLATWRRTPRR 412
QY 388 -AGLGAVYAALERMGLDGCVEDLRSRL 413
DB 413 EATLELLGRVLRDMDLLGCLDIEEAL 439

RESULT 10
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663-
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match 8.9%; Score 206.5; DB 6; Length 283;
Best Local Similarity 27.4%; Pred. No. 3.4e-09;
Matches 74; Conservative 28; Mismatches 119; Indels 49; Gaps 13;

QY 15 LLLVLLGARAQGTSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCP 74

Db 25 LYLFLGAPCY----APALPCKEDEYVPGSECCPKSGYRVKACAGELTG-TVCEPCP 79
QY 75 QDTFLAWENHN--SECARCOACDEQASQVALENCSAVADTRCGCKPGWVECVSOCSV 132
Db 80 PGYIIA---HNLGSLCKLQCMCDPAMGLRASRNCSTENAVCGCSPGFH-----CIV 129
QY 133 SSPFYQPCPLDCGALHRRHLL---CSRRTDGTCLPLGFYEHGDCVSCPTSTLGSCE 189
Db 130 QDGDHCAACRAYATSSPGQVQGGTESQDTLQNCPPGTFS-----PNTLEECQH 181
QY 190 --RCA-----AVCGWRQMFVVQVLLAGLVPLLLGAT--LTYVYHGWPH-----KPLVTA 236
Db 182 QTRCSMLVTKAGAGTSSSHVWVWFLSGSLVIVVCSVTGLIICVGRKPRGDVVKIVSV 241
QY 237 DEAGMEALTPPPATHLSPLDSANTLLAPPD 266
Db 242 QRKRQEA--EGEATVIEALQ-----APPD 263

RESULT 11
US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US2005025069eA1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; FILE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126.126
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1997-07-09
; PRIOR FILING DATE: 1997-03-04
; PRIOR FILING DATE: 1997-03-04
; PRIOR FILING DATE: 1997-02-07
; PRIOR FILING DATE: 1997-02-07
; PRIOR FILING DATE: 1997-01-23
; PRIOR FILING DATE: 1996-12-06
; PRIOR FILING DATE: 1996-12-06
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-126-126-2
Query Match 8.6%; Score 200.5; DB 7; Length 161;
Best Local Similarity 29.8%; Pred. No. 5.5e-09;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNSECARCOACDEQA 99
Db 11 HPQNNISCTCKCHKGYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 69
QY 100 SQVALENCASAVADTRCGCKPGWFEVC---QVSCVSSSPFYQPCPLDCGALHRRHRLCS 156
Db 70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSCLN-GTVH----LSCQ 119
QY 157 RRTDCGTCLPGYEHGDCVSCPTSTLGSCE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLCTKLC 155
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-126-126-2
Query Match 8.6%; Score 200.5; DB 7; Length 161;
Best Local Similarity 29.8%; Pred. No. 5.5e-09;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNSECARCOACDEQA 99
Db 11 HPQNNISCTCKCHKGYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 69
QY 100 SQVALENCASAVADTRCGCKPGWFEVC---QVSCVSSSPFYQPCPLDCGALHRRHRLCS 156
Db 70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSCLN-GTVH----LSCQ 119
QY 157 RRTDCGTCLPGYEHGDCVSCPTSTLGSCE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLCTKLC 155

RESULT 12
US-11-057-923-3
; Sequence 3, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Keige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: 30kDa TNF Inhibitor
US-11-057-923-3

Query Match 8.6%; Score 200.5; DB 7; Length 161;
Best Local Similarity 29.8%; Pred. No. 5.5e-09;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNSECARCOACDEQA 99
Db 11 HPQNNISCTCKCHKGYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 69
QY 100 SQVALENCASAVADTRCGCKPGWFEVC---QVSCVSSSPFYQPCPLDCGALHRRHRLCS 156
Db 70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSCLN-GTVH----LSCQ 119
QY 157 RRTDCGTCLPGYEHGDCVSCPTSTLGSCE--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLCTKLC 155

RESULT 13
US-11-182-946-7
; Sequence 7, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-7

Query Match 8.6%; Score 199.5; DB 7; Length 335;
Best Local Similarity 21.4%; Pred. No. 1.5e-08;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLPCCRGCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVA 103
Db 56 GQFCHKPPGPKKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRRLCDEGHGLEV 115
QY 104 LENCASAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCGALHRRHTRLLCSRRTDCG 163
Db 116 EINCTRTQNTKCRCKENFF-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYHGDGCVSCTSTLSCPCERCAAVCGWR-QMFWVQVLLAGLVVPLLLGATLY 222
Db 150 -----EHGI-1KECTLTSNTKCKEE-----GSRNLGWLCLLL-LPIPLIVWVRKE 194
QY 223 TYRHCHWPHKPLVTADAGMEALTPPATLSPDLSAHTL---LAPDSEKICTVOLVGN 279
Db 195 VQKTCRKH-----KENQG-----SHESPTLNPTETVAINLSVDLSKYITI----- 236
QY 280 SWTPGYPTEQALCPQVTSWDLPSRGLPAAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
Db 237 -----AGVMTLS----- 243
QY 340 DAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQOQYEMLKWRQ 384
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQ 283

RESULT 14

US-11-076-187-3
; Sequence 3, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-3

Query Match 8.6%; Score 199.5; DB 7; Length 669;

Best Local Similarity 21.4%; Pred. No. 3.1e-08;

Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLPCCRGCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVA 103

Db 56 GQFCHKPPGPKKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRRLCDEGHGLEV 115
QY 104 LENCASAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCGALHRRHTRLLCSRRTDCG 163
Db 116 EINCTRTQNTKCRCKENFF-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYHGDGCVSCTSTLSCPCERCAAVCGWR-QMFWVQVLLAGLVVPLLLGATLY 222
Db 150 -----EHGI-1KECTLTSNTKCKEE-----GSRNLGWLCLLL-LPIPLIVWVRKE 194
QY 223 TYRHCHWPHKPLVTADAGMEALTPPATLSPDLSAHTL---LAPDSEKICTVOLVGN 279
Db 195 VQKTCRKH-----KENQG-----SHESPTLNPTETVAINLSVDLSKYITI----- 236
QY 280 SWTPGYPTEQALCPQVTSWDLPSRGLPAAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
Db 237 -----AGVMTLS----- 243
QY 340 DAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQOQYEMLKWRQ 384
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQ 283

RESULT 15

US-11-185-878-3
; Sequence 3, Application US/11185878
; Publication No. US20050282217A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: PF379PID1
; CURRENT APPLICATION NUMBER: US/11/185,878
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/280,047
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 331
; TYPE: PRT
; ORGANISM: human
US-11-185-878-3

Query Match 8.5%; Score 197; DB 7; Length 331;

Best Local Similarity 21.1%; Pred. No. 2.3e-08;

Matches 72; Conservative 41; Mismatches 106; Indels 122; Gaps 11;

QY 48 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCQACDEQASQVALENC 107

Db 58 CHPCPPGPKKARDCTVNGDEPDVPCQEGKEYTDKAHFSKRCRRLCDEGHGLEVINC 117

QY 108 SAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCGALHRRHTRLLCSRRTDCGTCPLP 167

Db 118 TRQNTQNTKCRCKENFF-----CNSTVCEHCDPCTKC----- 147

QY 168 GFYEHGDGCVSCTSTLSCPCERCAAVCGWRQMFVQVLLAGLVVPLLLGATLYTYRHC 227

```
Db 148 ---EHGI-IKECTITSNTKCEE-----GSRNGWLCLLL--LPIPLIVWYKKEVQKTC 196
Qy 228 WPHKPLVTADAGMEALTPPPATHLSPLDSAHTL---LAPDSESEKICTVQLVGNWTPG 284
Db 197 RKHR-----KENQG-----SHESPTLNPETVAINLSDDVLSKYITTI----- 233
Qy 285 YPETQEALCFQVTVSWDQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPA 344
Db 234 -----AGVMTLS----- 240
Qy 345 RRWKEFVRTLGLREAEIEAVEVE-IGRFRDOQYEMLKRWQ 384
Db 241 -QVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNHQ 280
```

Search completed: March 20, 2006, 08:01:30
Job time : 29 secs

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|-------------------|
| | | | | | | |
| 1 | 338 | 81.8 | 65 | 2 | US-09-527-236A-24 | Sequence 24, Appl |
| 2 | 338 | 81.8 | 65 | 2 | US-09-756-85A-24 | Sequence 24, Appl |
| 3 | 338 | 81.8 | 65 | 2 | US-10-041-574-24 | Sequence 24, Appl |
| 4 | 338 | 81.8 | 65 | 2 | US-09-093-094-24 | Sequence 24, Appl |
| 5 | 155 | 37.5 | 78 | 2 | US-08-828-683A-23 | Sequence 23, Appl |
| 6 | 142 | 34.4 | 70 | 2 | US-09-159-277A-6 | Sequence 6, Appl |
| 7 | 142 | 34.4 | 70 | 2 | US-08-844-691A-6 | Sequence 6, Appl |
| 8 | 136.5 | 33.1 | 68 | 2 | US-09-527-236A-23 | Sequence 23, Appl |
| 9 | 136.5 | 33.1 | 68 | 2 | US-09-756-85A-23 | Sequence 23, Appl |
| 10 | 136.5 | 33.1 | 68 | 2 | US-10-041-574-23 | Sequence 23, Appl |
| 11 | 136.5 | 33.1 | 68 | 2 | US-09-093-094-23 | Sequence 23, Appl |
| 12 | 118 | 28.6 | 64 | 2 | US-08-894-626-3 | Sequence 3, Appl |
| 13 | 102.5 | 24.8 | 45 | 1 | US-08-219-237B-11 | Sequence 11, Appl |
| 14 | 83 | 20.1 | 67 | 2 | US-09-527-236A-26 | Sequence 26, Appl |
| 15 | 83 | 20.1 | 67 | 2 | US-09-756-85A-26 | Sequence 26, Appl |
| 16 | 83 | 20.1 | 67 | 2 | US-10-041-574-26 | Sequence 26, Appl |
| 17 | 83 | 20.1 | 67 | 2 | US-09-093-094-26 | Sequence 26, Appl |
| 18 | 73.5 | 17.8 | 41 | 1 | US-08-444-005-28 | Sequence 28, Appl |
| 19 | 70.5 | 17.1 | 77 | 2 | US-08-995-159-7 | Sequence 7, Appl |
| 20 | 70.5 | 17.1 | 77 | 2 | US-08-828-683A-27 | Sequence 27, Appl |
| 21 | 70.5 | 17.1 | 77 | 2 | US-09-545-605-7 | Sequence 7, Appl |
| 22 | 70.5 | 17.1 | 77 | 2 | US-09-056-383-1 | Sequence 1, Appl |
| 23 | 68 | 16.5 | 40 | 1 | US-08-444-005-22 | Sequence 22, Appl |
| 24 | 68 | 16.5 | 67 | 2 | US-09-527-236A-25 | Sequence 25, Appl |
| 25 | 68 | 16.5 | 67 | 2 | US-09-756-85A-25 | Sequence 25, Appl |
| 26 | 68 | 16.5 | 67 | 2 | US-10-041-574-25 | Sequence 25, Appl |
| 27 | 68 | 16.5 | 67 | 2 | US-09-093-094-25 | Sequence 25, Appl |

Genitz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24
Query Match 81.8%; Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 60
QY 69 VEDLR 73
DB 61 VEDLR 65
RESULT 3
US-10-041-574-24
Sequence 24, Application US/10041574
Patent No. 6919078
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24

PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
US-10-041-574-24
Query Match 81.8%; Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 60
QY 69 VEDLR 73
DB 61 VEDLR 65
RESULT 4
US-09-095-094-24
Sequence 24, Application US/09095094
Patent No. 6949358
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,094
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-094-24
Query Match 81.8%; Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 6e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQOQYEMLKRWQOQOQAGLGAVYAALERMGLDGC 60

100

COUNTRY: USA
ZIP: 94304-1000

STATE: CA
COUNTRY: USA
ZIP: 94304-1019

;
COUNTRY: USA
;
ZIP: 94304-1018
;

05

05

```

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/844,691A
/ FILING DATE: 21-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/416,379
/ FILING DATE: 03-APR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kohnsli, Antoinette F.
/ REGISTRATION NUMBER: 34,202
/ REFERENCE/DOCKET NUMBER: 203442107001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650)813-5600
/ TELEFAX: (650)494-0792
/ TELEX: 706141 MRSNFOERS SFO
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 70 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 11
/ OTHER INFORMATION: /note= "Leu is replaced by Asn for
/ OTHER INFORMATION: the point mutant hTNFR-1"
/ US-08-844-691A-6

Query Match 34.4%; Score 142; DB 2; Length 70;
Best Local Similarity 47.1%; Pred. No. 3.6e-11;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

Qy 9 RWKEFVRLGLGRAEIAEAVEIGR-PRDOQYEMLKRWQQQP---AGLGAVVAALERMG 64
Db 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQSMLATWRRRTPREATLELGRVLDM 60
Qy 65 LDGCVEDL 72
Db 61 LIGCLEDI 68

RESULT 8
US-09-527-236A-23
/ Sequence 23, Application US/09527236A
/ Patent No. 6358508
/ GENERAL INFORMATION:
/ APPLICANT: Ni, Jian
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Fan, Ping
/ APPLICANT: Gentz, Reiner L.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
/ FILE REFERENCE: PF375P1
/ CURRENT APPLICATION NUMBER: US/09/527,236A
/ CURRENT FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/052,991
/ PRIOR FILING DATE: 1997-06-11
/ PRIOR APPLICATION NUMBER: 09/095,094
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/126,019
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/134,220
/ PRIOR FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 68
/ TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-09-527-236A-23

Query Match      33.1%; Score 136.5; DB 2; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.8e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

Qy 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDQYEMLMKRWQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRRLGLSDHEIDRLQNGRCLREAQYSMLATWRRTRREATLELLGRVLRMDL 60

Qy 66 DGCVEDL 72
Db 61 LGCLEDI 67

RESULT 9
US-09-756-854-23
; Sequence 23, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Pan, Ping
; Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-756-854-23

Query Match      33.1%; Score 136.5; DB 2; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.8e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

Qy 9 RWKEFVRTGLREAEIEAVEVEIGR-FRDQYEMLMKRWQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRRLGLSDHEIDRLQNGRCLREAQYSMLATWRRTRREATLELLGRVLRMDL 60

Qy 66 DGCVEDL 72
Db 61 LGCLEDI 67

```

Db 61 LGCLEDI 67

RESULT 10

US-10-041-574-23
; Sequence 23, Application US/10041574
; Patent No. 6919078
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-23

Query Match 33.1%; Score 136.5; DB 2; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.8e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIIEAVEVEIGR-PRDQOYEMLKWRQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRRLGSLDHEIDRLQLONGRCLEAQSMLATWRRRTREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72
Db 61 LGCLEDI 67

RESULT 11

US-09-095-094-23
; Sequence 23, Application US/09095094
; Patent No. 6949358
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/095,094

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-094-23

Query Match 33.1%; Score 136.5; DB 2; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.8e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIIEAVEVEIGR-PRDQOYEMLKWRQ--QQPAGLGAVYAALERMGL 65
Db 1 RWKEFVRRLGSLDHEIDRLQLONGRCLEAQSMLATWRRRTREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72
Db 61 LGCLEDI 67

RESULT 12

US-08-894-626-3
; Sequence 3, Application US/08894626
; Patent No. 6355780
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BOLDIN, Mark P.
; VAPFOLOMEV, Eugene E.
; PANCER, Zeev
; METT, Igor
; GONCHAROV, Tanya M.
; WEINWURZEL, Henry
; TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,626
; FILING DATE: 09-Dec-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 112,742
; FILING DATE: 22-FEB-1995
; APPLICATION NUMBER: IL 115,289
; FILING DATE: 13-SEP-1995
; APPLICATION NUMBER: PCT/US96/02326
; FILING DATE: 15-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-894-626-3

Query Match 28.6%; Score 118; DB 2; Length 64;
Best Local Similarity 42.6%; Pred. No. 4.5e-08;
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;
Qy 10 WKPFVRLGLREAEIEAVEIGR-FRDOQYEMLKRWQOOPAGLVVAALERMG--- 64
Db 1 WKPFVRLGLSDHEIDRLQNGRCLEAQYSLATWRRTPRR-----EATLELGRVLR 56
Qy 65 ---LDGCV 69
Db 57 DHDLGLCL 64

RESULT 13
US-08-219-237B-11
; Sequence 11, Application US/08219237B
; Patent No. 5674546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: James W. Hellwege
; STREET: P.O. Box 2266 Bads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516762
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-219-237B-11

Query Match 24.8%; Score 102.5; DB 1; Length 45;
Best Local Similarity 51.2%; Pred. No. 3.1e-06;
Matches 21; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
Qy 11 KPFVRLGLREAEIEAVEIGR-FRDOQYEMLKRWQOOP 50
Db 1 KPFVRLGLSDHEIDRLQNGRCLEAQYSLATWRRTP 41

RESULT 14
US-09-527-236A-26
; Sequence 26, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-26

Query Match 20.1%; Score 83; DB 2; Length 67;
Best Local Similarity 33.3%; Pred. No. 0.0019;
Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;
Qy 10 WKPFVRLGLREAEIEAVEIGRFRDOQYEMLKRW--RQOOPAGLVVAALERMG 64
Db 2 WEPLMKRLGLMDNEIKVKAERAGHRDTLYTMLIKWVNTKGRDASVHTLLDALETLG 58

RESULT 15
US-09-756-854-26
; Sequence 26, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375

Page 7

TELEPHONE: 301-309-8504

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS

SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids

NAME: 07 amino acids
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
05450

US-09-156-854-26

Query Match 20.1%: Score 83: DB 2: Length 67:

Best Local Similarity 33.3%; Pred. No. 0.0019;

Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

10 WKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRW--RQQQPAGLGAVYAALERMG 64

[illegible]

Z WEFLMRKLG LMDNEIKVAKAEAGHRDTLYIMLIKWVNKTGRDASVHTLLDLETLG 58

Search completed: March 20, 2006, 08:04:05

Job time : 25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:03:18 ; Search time 23 Seconds
(without alignments)
334.667 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413
Sequence: 1 VMDVAPARKKEFVFTLGLR.....ERMGLDGCVEDLSRLQRP 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 26016

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 52.5 | 12.7 | 74 | 2 F71080 | hypothetical prote |
| 2 | 50.5 | 12.2 | 71 | 2 G69463 | conserved hypotet |
| 3 | 50.5 | 12.2 | 72 | 2 E69386 | hypothetical prote |
| 4 | 50.5 | 12.2 | 73 | 2 D69499 | conserved hypotet |
| 5 | 50.5 | 12.2 | 79 | 2 A84092 | hypothetical prote |
| 6 | 49.5 | 12.0 | 78 | 2 H84353 | hypothetical prote |
| 7 | 48 | 11.6 | 72 | 2 A82881 | conserved hypotet |
| 8 | 47 | 11.4 | 60 | 2 D83610 | hypothetical prote |
| 9 | 47 | 11.4 | 61 | 2 C69333 | hypothetical prote |
| 10 | 47 | 11.4 | 67 | 2 A96702 | unknown protein, 7 |
| 11 | 46.5 | 11.3 | 64 | 2 G83940 | hypothetical prote |
| 12 | 46.5 | 11.3 | 68 | 2 JH0129 | repressor protein |
| 13 | 46.5 | 11.3 | 79 | 2 A80619 | probable damage-in |
| 14 | 46 | 11.1 | 72 | 2 A75099 | hypothetical prote |
| 15 | 46 | 11.1 | 76 | 2 H70576 | hypothetical prote |
| 16 | 45.5 | 11.0 | 52 | 2 F83985 | hypothetical prote |
| 17 | 45 | 10.9 | 67 | 2 AC1037 | probable phage tai |
| 18 | 45 | 10.9 | 71 | 1 F70799 | integrase-related |
| 19 | 45 | 10.9 | 80 | 2 F72303 | glutaredoxin - The |
| 20 | 44.5 | 10.8 | 72 | 2 G91153 | host factor for ly |
| 21 | 44.5 | 10.8 | 72 | 2 C85999 | host factor for ly |
| 22 | 44.5 | 10.8 | 72 | 2 A49988 | slyx protein - Esc |
| 23 | 44.5 | 10.8 | 74 | 2 B75199 | hypothetical prote |
| 24 | 44 | 10.7 | 67 | 2 AG0927 | probable phage tai |
| 25 | 44 | 10.7 | 68 | 2 B55682 | keratin 15, type I |
| 26 | 44 | 10.7 | 70 | 2 F81899 | hypothetical prote |
| 27 | 43.5 | 10.5 | 62 | 2 F69871 | hypothetical prote |
| 28 | 43.5 | 10.5 | 75 | 2 AE2659 | conserved hypotet |
| 29 | 43.5 | 10.5 | 75 | 2 C97441 | hypothetical prote |

| | | | | | |
|----|------|------|----|----------|---------------------|
| 30 | 43 | 10.4 | 65 | 2 E70644 | probable ribosomal |
| 31 | 43 | 10.4 | 65 | 2 A90826 | lcd-like protein [|
| 32 | 43 | 10.4 | 65 | 2 H81238 | hypothetical prote |
| 33 | 43 | 10.4 | 71 | 2 T45384 | ribosomal protein |
| 34 | 43 | 10.4 | 73 | 2 F64547 | hypothetical prote |
| 35 | 43 | 10.4 | 77 | 2 F69219 | conserved hypotet |
| 36 | 42.5 | 10.3 | 47 | 2 I53270 | mineralocorticoid |
| 37 | 42.5 | 10.3 | 58 | 2 S60803 | M protein precursor |
| 38 | 42.5 | 10.3 | 77 | 2 A82086 | hypothetical prote |
| 39 | 42.5 | 10.3 | 79 | 2 F72592 | hypothetical prote |
| 40 | 42.5 | 10.3 | 80 | 2 S60835 | M protein precursor |
| 41 | 42 | 10.2 | 37 | 2 D69283 | conserved hypotet |
| 42 | 42 | 10.2 | 61 | 2 AD2769 | hypothetical prote |
| 43 | 42 | 10.2 | 73 | 2 H83960 | hypothetical prote |
| 44 | 42 | 10.2 | 77 | 2 D81212 | 50S ribosomal prot |
| 45 | 41.5 | 10.0 | 36 | 2 C69327 | hypothetical prote |

ALIGNMENTS

RESULT 1

F71080
hypothetical protein PHS027 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: F71080
R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71080
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-74 <KAW>
A;Cross-references: UNIPROT:O73992; UNIPARC:UPI0000062CAA; GB:AP000004; NID:93236131; PII
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetic:
A;Gene: PHS027

Query Match 12.7%; Score 52.5; DB 2; Length 74;
Best Local Similarity 27.3%; Pred. No. 81;
Matches 18; Conservative 14; Mismatches 27; Indels 7; Gaps 2;

| | | | |
|----|----|---|----|
| QY | 5 | VPARRWKEFVFTLGLREAEIEAVEVEIGRFRDQOQYEMLXWRQOQAGLGAATVAAERMG | 64 |
| DB | 14 | IPA-----EIRKALGKSGELLEVKGLEDGKI---IIBRLKKRKTLLKGLKLTPEIEKAI | 66 |
| QY | 65 | LDGCVE | 70 |
| DB | 67 | VEGMKE | 72 |

RESULT 2

G69463
conserved hypothetical protein AF1712 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69463
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69463
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-71 <KLE>

Result No. Score Query Match Length DB ID Description

A;Cross-references: UNIPROT:O28561; UNIPARC:UPI0000056C07; GB:AE000985; GB:AE000782; NID
C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975

Query Match 12.2%; Score 50.5; DB 2; Length 71;
Best Local Similarity 32.7%; Pred. No. 1.3e+02;
Matches 16; Conservative 10; Mismatches 18; Indels 5; Gaps 1;

Qy 1 VMDAPVARRKVEFRTTGLREAEIEAVEVE-----IGRFDDQYEMLKR 44
Db 4 IIEAVYQGVKPLRKVSLREGEIVKVEITRTKVTGTFYAKLRELEKR 52

RESULT 3
E69386
hypothetical protein AF1094 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69386
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69386
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-72 <KLE>
A;Cross-references: UNIPROT:O29171; UNIPARC:UPI0000056E76; GB:AE001028; GB:AE000782; NID

Query Match 12.2%; Score 50.5; DB 2; Length 72;
Best Local Similarity 27.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 12; Mismatches 26; Indels 1; Gaps 1;

Qy 11 KEFRTTGLREAEIEAVEVEIGRFDDQY-EMLKRFQQQAGVAVYALERM 63
Db 12 ENFIRQLEKRGGELEELKDELITFSDAEFIDSIQGLSLDEQGRSKVCSNLEEV 65

RESULT 4
D69499
conserved hypothetical protein AF1997 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69499
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69499
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-73 <KLE>
A;Cross-references: UNIPROT:O28282; UNIPARC:UPI0000056AFA; GB:AE000965; GB:AE000782; NID
C;Superfamily: uncharacterized conserved protein

Query Match 12.2%; Score 50.5; DB 2; Length 73;
Best Local Similarity 27.7%; Pred. No. 1.3e+02;
Matches 13; Conservative 8; Mismatches 19; Indels 7; Gaps 1;

Qy 8 RRFVEFRTTGLREAEIEAVEVEIGRFDDQYEMLKR-----WRQ 47
Db 22 RSFSEVIRELVKSGNFLLMVAFTGRSEEVKLRKEMKEVEEWMQ 68

RESULT 5
A84092

hypothetical protein BH3537 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84092
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84092
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
A;Cross-references: UNIPROT:Q9K736; UNIPARC:UPI00000C4224; GB:AP001519; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3537

Query Match 12.2%; Score 50.5; DB 2; Length 79;
Best Local Similarity 27.6%; Pred. No. 1.4e+02;
Matches 16; Conservative 12; Mismatches 15; Indels 15; Gaps 2;

Qy 21 EAEIEAVEVEIGRFDDQYEMLKRQQQAGVAVYALERMGLDGCVEDLRSRLR 78
Db 34 KAALREALHSEFGFGKKRQARFMKAFKQK-----VYEII-----VEEKRLQR 76

RESULT 6
H84353
hypothetical protein Vng2035h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84353
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: H84353
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-78 <STO>
A;Cross-references: UNIPROT:Q9HN4; UNIPARC:UPI0000063A22; GB:AE004437; NID:GI0581461; P
C;Genetics:
A;Gene: VNG2035H

Query Match 12.0%; Score 49.5; DB 2; Length 78;
Best Local Similarity 27.8%; Pred. No. 1.8e+02;
Matches 15; Conservative 7; Mismatches 23; Indels 9; Gaps 1;

Qy 23 EIEAVEVEIGRFDDQYEMLKRQQQAGVAVYALERMGLDGCVEDLRSRL 76
Db 33 DADGTWEVDVERDGSYEVVASWNAD-----GDLADVAVPAYVEDLLSRL 77

RESULT 7
A82881
conserved hypothetical U0518 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82881
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: A82881
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <GLA>
A;Cross-references: UNIPARC:UPI00000C1CA2; GB:AE002150; GB:AF222894; NID:G6899515; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:


```

unknown protein, 70659-70456 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A96702
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <STO>
A;Cross-references: UNIPROT:Q9CV8; UNIPARC:UPI00000A8C1A; GB:AE005173; NID:g6553903; PII
C;Genetics:
A;Gene: T23K23.23
A;Map position: 1

Query Match 11.4%; Score 47; DB 2; Length 67;
Best Local Similarity 34.8%; Pred. No. 2.9e+02;
Matches 16; Conservative 5; Mismatches 13; Indels 12; Gaps 2;

Qy 11 KEF--VRTLGLRAEIEAIVEVEIGRFRDQQYEMLKRWRQQQAPGLG 54
||| | | | | | | | | | | | | | |
Db 24 KEFEKIRQPSLQQPMRRVLSEIKR-----RQRSRPLGLG 59

```

RESULT 11

G83940

hypothetical protein BH2327 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: G83940

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maqui, N.; Fujii, P.; Hirano

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: AB83650; MUID: 20512582; PMID:11058132
A;Accession: G83940
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <STO>
A:Cross-references: UNIPROT:Q9KAGO; UNIPARC:UIPI0000C3E9B; GB:AP001515; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
C:Gene: BR2327

Query Match 11.3%; Score 46.5; DB 2; Length 64;
Best Local Similarity 31.8%; Pred. No. 3.le+02;
Matches 14; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 19 LREAIEAVEVE-----IGFRDQQVEMLKRWRCQQPAGLGAVY 57
|||:::||::||::||::||::||::||::||::||::||::||::||
Db 13 LRDGELSVRIEKNDPLIFRQVLAEQDMKSFERNAGRGGGVIV 56

RESULT 12
JH0129
repressor protein cac - Escherichia coli plasmid RSP1010
N/Alternate names: repressor protein P
C/Species: Escherichia coli
A/Note: plasmid RSP1010 is a broad-host-range plasmid belonging to incompatibility group C.
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: JH0129, #seq292

Gene 75, 271-288, 1989
A+Title: Complete nucleotide sequence and gene organization of the broad-host-range plasm
A+Reference number: J01033. M100.8032759. SWIN.2651065

RESULT 14
A75099
hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: A75099
C.Annotation: Genoscope
submitted to the EMBL Data Library, July 1999
A.Description: Pyrococcus abyssi Genome sequence: insights into archaeal chromosome str
A.Reference number: A75001
A.Accession: A75099
A.Status: preliminary

Search completed: March 20, 2006, 08:05:27
Job time : 25 secs

A;Status: preliminary

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|--------|-------------|
| | Score | Match | Length | | | |
| 1 | 60.5 | 14.6 | 79 | 2 | Q52130 | NOCFA |
| 2 | 59 | 14.3 | 79 | 2 | Q93R97 | PSPPU |
| 3 | 57 | 13.8 | 55 | 2 | Q6TG30 | AZOMA |
| 4 | 56.5 | 13.7 | 72 | 2 | Q5J162 | PYROCCU |
| 5 | 54.5 | 13.2 | 59 | 2 | Q7P3Z1 | FUSNV |
| 6 | 54 | 13.1 | 69 | 2 | Q9ZXL9 | 9CAUD |
| 7 | 54 | 13.1 | 78 | 2 | Q4ZBG0 | 9VIRU |
| 8 | 54 | 13.1 | 78 | 2 | Q6CZU0 | ERWCT |
| 9 | 53.5 | 13.0 | 79 | 2 | Q8FYAS | METKA |
| 10 | 53 | 12.8 | 62 | 2 | Q5SM18 | THEB8 |
| 11 | 53 | 12.8 | 62 | 2 | Q7ZGH9 | THEFT2 |
| 12 | 53 | 12.8 | 75 | 2 | Q8U397 | PYRFX |
| 13 | 53 | 12.8 | 78 | 2 | Q7U9X2 | SYNPK |
| 14 | 52.5 | 12.7 | 70 | 2 | Q8H4R5 | ORYZA |
| 15 | 52.5 | 12.7 | 74 | 2 | Q73992 | PYRHO |
| 16 | 52.5 | 12.7 | 77 | 2 | Q6PX14 | STAXY |
| 17 | 52 | 12.6 | 70 | 2 | Q93NF5 | ARTNI |
| 18 | 52 | 12.6 | 80 | 2 | Q41VR1 | AZOV1 |
| 19 | 51.5 | 12.5 | 80 | 2 | Q5QK7 | 9CAUD |
| 20 | 51 | 12.3 | 55 | 2 | Q5G510 | AZOSA |
| 21 | 51 | 12.3 | 66 | 2 | Q8AU2 | PSESM |
| 22 | 51 | 12.3 | 73 | 2 | Q5VPA4 | ORYSA |
| 23 | 50.5 | 12.2 | 57 | 2 | Q5UXU2 | HALMA |
| 24 | 50.5 | 12.2 | 63 | 2 | Q5SM75 | 9CAUD |
| 25 | 50.5 | 12.2 | 63 | 2 | Q7EYN4 | ORYSA |
| 26 | 50.5 | 12.2 | 70 | 2 | Q7V7D7 | PROMM |
| 27 | 50.5 | 12.2 | 71 | 1 | Y112 | ARCFU |
| 28 | 50.5 | 12.2 | 72 | 1 | Y1094 | ARCFU |
| 29 | 50.5 | 12.2 | 73 | 1 | Y1997 | ARCFU |
| 30 | 50.5 | 12.2 | 61 | 2 | Q87D36 | BACHD |
| 31 | 50 | 12.1 | 61 | 2 | Q8QD62 | VIBVU |

```

AC OSJ162;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
DE OrderedLocustNames=TK0923;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae
OC Thermococcus.
OX NCBI_TaxId=69014;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RR STRAIN=KOD1;
RC PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Acomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT genomes."
RL Genome Res. 15:352-363 (2005).
DR EMBL; AP006878; BAD85112.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 72 AA; 8420 MW; 605AF03D9F66F69F CRC64;

Query Match 13.7%; Score 56.5; DB 2; Length 72;
Best Local Similarity 34.7%; Pred. No. 3e+02;
Matches 17; Conservative 11; Mismatches 12; Indels 9; Gaps

Qy 1 VMDAVPARRWK-EFV---RTGLRRAETEA-VEVEIGRFRDQOYEMLKR 44
Db 23 VKRAETEARIEFIEDIARRGLDKEIDAEI- ---KARDEAWQEFKK 67

RESULT 5
Q7P321_FUSNV
AC Q7P321_FUSNV PRELIMINARY; PRT; 59 AA.
ID Q7P321;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Virulence-associated protein I.
GN Name=PNV0340;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxId=209882;
[1]
RP NUCLEOTIDE SEQUENCE.
RR STRAIN=ATCC 49256;
RC Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haelkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABF01000154; EAA23321.1; -; Genomic DNA.
DR SQ SEQUENCE 59 AA; 6808 MW; 615C5DF19B31BE86 CRC64;

Query Match 13.2%; Score 54.5; DB 2; Length 59;
Best Local Similarity 37.2%; Pred. No. 4e+02;
Matches 16; Conservative 5; Mismatches 21; Indels 1; Gaps

Qy 11 KEFVRTGLRRAETEA-VEVEIGRFRDQOYEMLKWQOQPAG 52
Db 9 KGMVQLGLPEKLETALINAEISISHDMIYRIVKTMHQKNYG 51

RESULT 6
Q9ZXU9_9CAUD
AC Q9ZXU9_9CAUD PRELIMINARY; PRT; 69 AA.
ID Q9ZXU9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
 OS Bacteriophage phi CTX.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P2-like viruses.
 OX NCBI_TaxID=35343;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=phiCTX-C;
 RX MEDLINE=90014160; PubMed=2507866;
 RA Hayaishi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
 RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene
 and the mechanism of activation of the protoxin.";
 RL Mol. Microbiol. 3:861-868(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=phiCTX-C;
 RX MEDLINE=99157549; PubMed=10027959;
 RA Nakayama K., Kanaya S., Onishi M., Terawaki Y., Hayashi T.;
 RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
 phage of Pseudomonas aeruginosa: implications for phage evolution and
 RT horizontal gene transfer via bacteriophage.";
 RL Mol. Microbiol. 31:399-419(1999).
 DR EMBL; AB008550; BAA36234.1; -; Genomic_DNA.
 DR InterPro; IPR008861; Tail_X.
 DR Pfam; PF05489; Phage tail X; 1.
 SQ SEQUENCE 69 AA; 7436 MW; D2E35A698F195CC0 CRC64;

 Query Match 13.1%; Score 54; DB 2; Length 69;
 Best Local Similarity 45.8%; Pred. No. 5.3e+02;
 Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

 QY 3 DAVPARRWKEFVRTGLREAEIA 26
 DB 10 DTVEALCWRYHGTAGTVEAVLEA 33

 RESULT 7
 Q4ZBG0_9VIRU
 ID Q4ZBG0_9VIRU PRELIMINARY; PRT; 78 AA.
 AC Q4ZBG0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE ORF067.
 OS Bacteriophage 71.
 OC Viruses.
 OX NCBI_TaxID=320844;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=phiCTX-C;
 RX PubMed=15788529; DOI=10.1073/pnas.0501140102;
 RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
 RT "The complete genomes and proteomes of 27 Staphylococcus aureus
 RT bacteriophages.";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
 DR EMBL; AY954962; AAX91625.1; -; Genomic_DNA.
 SQ SEQUENCE 78 AA; 8987 MW; 1383AFA7A3A06887 CRC64;

 Query Match 13.1%; Score 54; DB 2; Length 78;
 Best Local Similarity 31.2%; Pred. No. 6e+02;
 Matches 20; Conservative 10; Mismatches 28; Indels 6; Gaps 3;

 QY 17 LGLEAEIAEAVEIGRFRDQYQYMLK-RWRQQQPAGLGAAYALERMGLDG----CVD 71
 DB 12 MALKEHNKLTSEIGVNRDTLSNMTHGRTKPSYFV-INGIYFALBELTPQEGRDIFNED 70

 QY 72 LRSR 75
 DB 71 LRKK 74

 RESULT 8
 Q6CZU0_ERWCT

ID Q6CZU0_ERWCT PRELIMINARY; PRT; 78 AA.
 AC Q6CZU0;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=EC4061;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jags K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 DR EMBL; BX950851; CAG76958.1; -; Genomic_DNA.
 DR InterPro; IPR008227; UCP006169.
 DR InterPro; IPR010648; UPF0270.
 DR Pfam; PF06794; UPF0270; 1.
 DR PIRSF; PIRSF006169; UCP006169; 1.
 KW Complete proteome, Hypothetical protein.
 SQ SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12BF9C CRC64;

 Query Match 13.1%; Score 54; DB 2; Length 78;
 Best Local Similarity 36.0%; Pred. No. 6e+02;
 Matches 18; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

 QY 41 MLKRWKQQQAPGL-----GAVYAALERMGLDGCVDLRSRLQRG 79
 DB 1 MIIPWQLDPTLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSLOQS 49

 RESULT 9
 Q8TYA5_METKA
 ID Q8TYA5_METKA PRELIMINARY; PRT; 79 AA.
 AC Q8TYA5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Predicted RNA-binding protein containing the S4 domain.
 GN OrderedLocusNames=MK0398;
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_TaxID=2320;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natile D.A., Rogosin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozaykhan S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 DR EMBL; AE010336; AAM01613.1; -; Genomic_DNA.
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR InterPro; IPR002942; S4.
 DR Pfam; PF01479; S4; 1.
 DR SMART; SM00363; S4; 1.

DR PROSITE; P50889; S4; 1.
KW Complete proteome; RNA-binding.
SQ SEQUENCE 79 AA; 8930 MW; 87B143AA16BAF785 CRC64;

Query Match 13.0%; Score 53.5; DB 2; Length 79;
Best Local Similarity 32.4%; Pred. No. 6.1e+02;
Matches 22; Conservative 7; Mismatches 26; Indels 13; Gaps 3;

QY 8 RRWKEFVRTGLREAEIEA-VEIGRFRDQQOYEMLKRWKROQPAGLGAVYAALERMGLD 66
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
DB 5 RRLDAFLRDVGLAESPREAKRLVSGSRVRVNGKLVKPFWLVSPG-----DEIENV 55

QY 67 GC---VED 71
|-|-|-|
DB 56 GVTVRVED 63

RESULT 10
ID QSM18_THET8 PRELIMINARY; PRT; 62 AA.
AC QSM18;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein TTHA0125.
GN OrderedLocusNames=TTHA0125;
OS Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermoales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=300852;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HB8;
RA Masui R., Kurokawa K., Nakagawa N., Tokunaga F., Koyama Y., Shibata I., Oshima T., Yokoyama S., Yasunaga T., Kuramitsu S.;
RT "Complete genome sequence of Thermus thermophilus HB8."
RL Submitted (NOV-2004) to the EMBL/GenBank/DDJ databases.
DR EMBL; AP008226; BAD69948.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;

Query Match 12.8%; Score 53; DB 2; Length 62;
Best Local Similarity 29.3%; Pred. No. 6.1e+02;
Matches 17; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

QY 8 RRWKEFVRTGLREAEIEA-VEIGRFRDQQOYEMLKRWKROQPAGLGAVYAALERMGM 64
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
DB 4 RRLKSVESQARIREHQAKIEELRR--PEPRWELIRYWEKIIRTPGRVERLLRRMG 60

RESULT 11
ID Q72GH9_THET2 PRELIMINARY; PRT; 62 AA.
AC Q72GH9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TC1869;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermoales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15064768; DOI=10.1038/nbt956;
RA Henne A., Brueggemann H., Raasch C., Wiesz A., Hartisch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacob C., Starkuviene V., Schlenczek S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus thermophilus."
RL Nat. Biotechnol. 22:547-553(2004).

DR ENBL; AE017307; AAS82211.1; -: Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;

Query Match 12.8%; Score 53; DB 2; Length 62;
Best Local Similarity 29.3%; Pred. No. 6.1e+02;
Matches 17; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

QY 8 RRWKEFVRTGLREAEIEA-VEIGRFRDQQOYEMLKRWKROQPAGLGAVYAALERMGM 64
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
DB 4 RRLKSVESQARIREHQAKIEELRR--PEPRWELIRYWEKIIRTPGRVERLLRRMG 60

RESULT 12
ID Q8U397_PYRFU PRELIMINARY; PRT; 75 AA.
AC Q8U397;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PF0573.
GN OrderedLocusNames=PF0573;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DDJ databases.
DR EMBL; AE010180; AAL80697.1; -; Genomic DNA.
DR InterPro; IPRO06339; AbzB trans reg.
DR InterPro; IPRO07159; SpoVT_AbrB.
DR Pfam; PF04014; SpoVT_AbrB; 1.
DR TIGRFAMs; TIGR01439; lp_hmg_hel_AbrB; 1.
KW Complete proteome.
SQ SEQUENCE 75 AA; 8705 MW; 6FE2F4AF7D807146 CRC64;

Query Match 12.8%; Score 53; DB 2; Length 75;
Best Local Similarity 28.6%; Pred. No. 7.4e+02;
Matches 20; Conservative 14; Mismatches 24; Indels 12; Gaps 4;

QY 5 VPARRWKVFVRTGLREAEIEA-VEIGRFRDQQOYEMLKRWKROQPAG----LGAVYAAL 60
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
DB 14 IPA----EIKALGIKEGELLEVLRLNGKI---IIERLKKERKTILKLGKLTLEIEIAI 66

QY 61 ERMLDGCVBE 70
|-|-|-|
DB 67 EE-GMKQCQM 75

RESULT 13
ID Q7U9X2_SYNPX PRELIMINARY; PRT; 78 AA.
AC Q7U9X2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=SYNW0130;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsa B., Larimer P.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., Paulsen I.T., Dufresne A., Fartensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus."
RL Nature 424:1037-1042(2003).

Search completed: March 20, 2006, 08:04:59
Job time : 108 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:02:39 ; Search time 79 Seconds
(without alignments)

444.941 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRLTGLR.....ERMGLDGVEDLRSLRQRP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1293556

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_21.*

2: Geneseqp1980s.*

3: Geneseqp1990s.*

4: Geneseqp2000s.*

5: Geneseqp2001s.*

6: Geneseqp2002s.*

7: Geneseqp2003s.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 381 | 92.3 | 74 | 5 | ABG31492 Human Apo |
| 2 | 381 | 92.3 | 74 | 7 | ADG98744 Apo-3/DR3 |
| 3 | 381 | 92.3 | 74 | 8 | ADO40453 Human Apo |
| 4 | 338 | 81.8 | 65 | 2 | AAW93610 Human DR3 |
| 5 | 338 | 81.8 | 65 | 3 | AAW93610 Human DR3 |
| 6 | 155 | 37.5 | 78 | 5 | ABG31493 Human Apo |
| 7 | 155 | 37.5 | 78 | 6 | ADA49709 Death dom |
| 8 | 155 | 37.5 | 78 | 7 | ADG98745 TNFR1 dea |
| 9 | 155 | 37.5 | 78 | 8 | ADO40454 Human TNF |
| 10 | 142 | 34.4 | 69 | 2 | AAW93612 Human TNF |
| 11 | 139 | 33.7 | 30 | 4 | AAO08695 Human pol |
| 12 | 136.5 | 33.1 | 68 | 3 | AAW93612 Human TNF |
| 13 | 118 | 28.6 | 64 | 2 | AAW00208 Human p55 |
| 14 | 105 | 25.4 | 75 | 7 | ADG42594 NOV1 doma |
| 15 | 94 | 22.8 | 76 | 8 | ADO40451 Human Apo |
| 16 | 83 | 20.1 | 67 | 3 | AAW93613 Human DR5 |
| 17 | 82 | 19.9 | 67 | 2 | AAW93613 Human CAR |
| 18 | 77.5 | 18.8 | 67 | 3 | AAW93613 Human CAR |
| 19 | 74 | 17.9 | 45 | 4 | AAW93613 Human CAR |
| 20 | 74 | 17.9 | 45 | 4 | AAW93613 Human CAR |
| 21 | 74 | 17.9 | 45 | 4 | AAW93613 Human CAR |
| 22 | 70.5 | 17.1 | 77 | 6 | ADA49713 Death dom |
| 23 | 68 | 16.5 | 67 | 3 | AAW93613 Human CAR |
| 24 | 67 | 16.2 | 51 | 2 | AAW93613 Human CAR |

| | | | | | | |
|----|------|------|----|---|----------|--------------------|
| 25 | 64.5 | 15.6 | 65 | 5 | AAE24868 | AAE24868 Chlamydia |
| 26 | 64.5 | 15.6 | 65 | 5 | AAE38911 | AAE38911 Chlamydia |
| 27 | 60 | 14.5 | 77 | 2 | AAW62177 | AAW62177 Nerve gro |
| 28 | 60 | 14.5 | 77 | 8 | ADJ25858 | ADJ25858 Nerve gro |
| 29 | 60 | 14.5 | 77 | 9 | ADZ48605 | ADZ48605 Nerve gro |
| 30 | 57.5 | 13.9 | 63 | 2 | AAW00206 | AAW00206 Human Fas |
| 31 | 57.5 | 13.9 | 68 | 2 | AAW93611 | AAW93611 Human Fas |
| 32 | 57.5 | 13.9 | 68 | 3 | AAW93611 | AAW93611 Human Fas |
| 33 | 57.5 | 13.9 | 68 | 4 | AAW93611 | AAW93611 Human Fas |
| 34 | 57.5 | 13.9 | 77 | 6 | ABG31494 | ABG31494 Human Apo |
| 35 | 57.5 | 13.9 | 77 | 7 | ADA49710 | ADA49710 Death dom |
| 36 | 57.5 | 13.9 | 77 | 7 | ADG98746 | ADG98746 Fas/Apo1 |
| 37 | 57.5 | 13.9 | 77 | 8 | ADO40455 | ADO40455 Human Fas |
| 38 | 57 | 13.8 | 65 | 5 | AAE24866 | AAE24866 Chlamydia |
| 39 | 57 | 13.8 | 65 | 5 | AAE38909 | AAE38909 Chlamydia |
| 40 | 57 | 13.8 | 71 | 5 | AAE24857 | AAE24857 Mouse NGF |
| 41 | 57 | 13.8 | 71 | 5 | AAE38900 | AAE38900 Mouse NGF |
| 42 | 56.5 | 13.7 | 73 | 8 | ADN46273 | ADN46273 Thermococ |
| 43 | 56 | 13.6 | 65 | 5 | AAE24856 | AAE24856 Chlamydia |
| 44 | 56 | 13.6 | 65 | 5 | AAE38899 | AAE38899 Chlamydia |
| 45 | 55 | 13.3 | 60 | 4 | AAU63529 | AAU63529 Propionib |

ALIGNMENTS

RESULT 1

ABG31492

ID ABG31492 standard; protein; 74 AA.

XX AC ABG31492;

XX AC

DT 21-NOV-2002 (first entry)

XX

DE Human Apo-2Dcr associated protein #2.

XX

KW Human; Apo-2Dcr; Apo-2 ligand; programmed cell death; apoptosis;

KW neurodegenerative disease; autoimmune; inflammatory.

XX

OS Homo sapiens.

XX

PN US2002102706-A1.

XX

PD 01-AUG-2002.

XX

PF 21-JUN-2001; 2001US-00887879.

XX

PR 18-JUN-1997; 97US-0049911P.

PR 12-JUN-1998; 98US-00096500.

XX

(GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;

PI Wood WI;

DR WPI; 2002-697823/75.

XX

PT Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in

PT mammalian cells.

XX

PS Disclosure; Page 37; 58pp; English.

XX

CC The present invention relates to the isolation of novel human

CC polypeptides, designated Apo-2Dcr, and the polynucleotide sequences

CC encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is useful

CC for modulating programmed cell death or apoptosis in mammalian cells. Apo

CC -2Dcr can be used to produce apo-2Dcr antibodies which are useful.

CC therapeutically, and can cross-react with other receptors for Apo-2

CC ligand to block excessive apoptosis in neurodegenerative diseases, or to

CC block potentially autoimmune or inflammatory effects. Apo-2Dcr antibodies

CC are also useful in immunohistochemistry staining assays or diagnostic

CC assays for Apo-2Dcr, e.g. detecting its expression in specific cells,

CC tissues or serum, and for the affinity purification of Apo-2Dcr from

CC recombinant cell culture or natural sources. The present sequence
 CC represents a protein of unknown function relating to the present
 CC invention. Note: The present sequence is given in the Seq listing but is
 CC not mentioned elsewhere in the specification
 XX
 SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 5; Length 74;
 Best Local Similarity 100.0%; Pred. No. 5.8e-41;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60
 DB 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
 DB 61 ERMGLDGCVEDLRS 74

RESULT 2
 ADG98744
 ID ADG98744 standard; protein; 74 AA.
 AC ADG98744;
 DT 11-MAR-2004 (first entry)
 DE Apo-3/DR3 death domain protein.
 KW Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
 KW cancer; gene therapy.
 XX Unidentified.
 XX US2003148455-A1.
 XX 07-AUG-2003.
 XX 06-NOV-2002; 2002US-00288917.
 XX 15-MAY-1997; 97US-0046615P.
 XX 09-FEB-1998; 98US-0074119P.
 XX 14-MAY-1998; 98US-00079029.
 XX 02-NOV-2001; 2001US-00052798.
 XX (GETH) GENENTECH INC.
 PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 PI WPI; 2003-897574/82.
 DR New Apo-2 polypeptide or its extracellular or death domain sequence,
 XX useful for modulating apoptosis in mammalian cancer cells or for
 XX generating transgenic or knockout animals.
 XX Disclosure; Fig 2B; 64pp; English.

XX The present invention provides novel Apo-2 protein and the nucleic acid
 CC encoding the protein. The invention is useful in inducing apoptosis in
 CC mammalian cancer cells. The invention is also useful in diagnostic
 CC procedures for tissue-specific typing and in generating transgenic
 CC animals that are useful in development and screening of reagents. The
 CC invention is also useful in gene therapy. The present sequence is
 CC Apo3/DR3 death domain protein.
 XX
 SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 7; Length 74;
 Best Local Similarity 100.0%; Pred. No. 5.8e-41;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60

DB 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60
 QY 61 ERMGLDGCVEDLRS 74
 DB 61 ERMGLDGCVEDLRS 74

RESULT 3
 ADO40453
 ID ADO40453 standard; protein; 74 AA.
 XX ADO40453;
 AC ADO40453;
 DT 15-JUL-2004 (first entry)
 DE Human Apo-3/DR3 protein.
 XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
 KW gene therapy; human; Apo-3/DR3.
 XX Homo sapiens.
 XX US2004003552-A1.
 XX 15-JAN-2004.
 XX 25-APR-2003; 2003US-00423448.
 XX 15-MAY-1997; 97US-0046615P.
 XX 09-FEB-1998; 98US-0074119P.
 XX 14-MAY-1998; 98US-00079029.
 XX 02-NOV-2001; 2001US-00052798.
 XX 06-NOV-2002; 2002US-00288917.
 XX (GETH) GENENTECH INC.
 PA Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
 PI WPI; 2004-090468/09.
 DR New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
 XX diagnosing, preventing or treating cancer, and in tissue typing or in
 XX generating antibodies or transgenic animals.
 XX Example 1; Fig 2B; 53pp; English.

XX The present invention provides novel Apo-2 polypeptide and the encoding
 CC polynucleotide capable of modulating apoptosis. The invention is useful
 CC in diagnosing, treating and preventing cancer, tissue typing, in
 CC generating antibodies and transgenic animals. The invention is also
 CC useful in gene therapy. The present sequence is human Apo-3/DR3 protein.
 CC This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 8; Length 74;
 Best Local Similarity 100.0%; Pred. No. 5.8e-41;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60
 DB 1 VMDAVPARRWKKEFVRLTGLREAEIEAVEVEIGRFRDQOYEMLKRWKQQPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
 DB 61 ERMGLDGCVEDLRS 74

RESULT 4
 AAW93610
 ID AAW93610 standard; protein; 65 AA.
 XX

AC AAW93610;
 XX 18-JUN-1999 (first entry)
 XX Human DR3 protein fragment.
 XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;
 KW p53-inducible; apoptosis-mediating activity; treatment; animal model;
 KW neoplastic disease; DR3.
 XX
 OS Homo sapiens.
 XX WO9902653-A1.
 XX 21-JAN-1999.
 XX 10-JUL-1998; 98WO-US014495.
 XX 11-JUL-1997; 97US-0052305P.
 PR 04-AUG-1997; 97US-0054710P.
 PR 30-SEP-1997; 97US-0060473P.
 PR 11-MAR-1998; 98US-0077526P.
 PR 11-MAR-1998; 98US-0077628P.
 PR 11-MAR-1998; 98US-0077661P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 XX El-Deiry WS;
 XX WPI; 1999-120857/10.
 XX
 XX A new nucleic acid encodes a p53-induced protein (Killer) - which induces
 PT apoptosis and is useful in the diagnosis and treatment of neoplastic
 PT diseases.
 XX
 PS Disclosure; Page 46; 65pp; English.
 XX
 CC This invention describes a novel human adriamycin-inducible killer
 CC protein located on chromosome 8p21, which also has p53-inducible,
 CC apoptosis-mediating activity and comprises an amino-terminal
 CC extracellular receptor, transmembrane and death domains. The nucleic acid
 CC molecule which encodes the protein, it's encoded signal transduction
 CC protein and antibodies of the invention are useful in the diagnosis and
 CC treatment of neoplastic diseases. The invention is also useful for the
 CC production of animal model systems
 XX
 SQ Sequence 65 AA;
 Query Match 81.8%; Score 338; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.7e-35;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRRQOQPAGLGAVYAALERMGLDGC 68
 DB 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRRQOQPAGLGAVYAALERMGLDGC 60
 QY 69 VEDLR 73
 DB 61 VEDLR 65
 RESULT 5
 ID AAB26990
 XX AAB26990 standard; protein; 65 AA.
 AC AAB26990;
 XX
 XX 02-FEB-2001 (first entry)
 XX Human DR3 death domain.
 XX Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
 KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
 KW

KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
 KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
 KW common variable immunodeficiency; X-linked agammaglobulinemia;
 KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
 KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
 KW cardiovascular disease; neurological disease; protein coordinate data;
 KW osteoprotegerin; DR3.
 XX
 OS Homo sapiens.
 XX WO200056862-A1.
 XX 28-SEP-2000.
 XX 16-MAR-2000; 2000WO-US006831.
 XX 24-MAR-1999; 99US-0126019P.
 PR 14-MAY-1999; 99US-0134220P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 FI Ni J, Gentz RL, Yu G, Fan P;
 XX WPI; 2000-594575/56.
 XX
 XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
 PT known as TR9, useful for treating, preventing and diagnosing severe
 PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
 PT and cancer.
 XX
 PS Disclosure; Fig 4C; 220pp; English.
 XX
 CC The present sequence is the death domain of DR3. It was used for
 CC comparison to a domain of a novel human tumour necrosis factor receptor,
 CC designated TR9. The TR9 receptor is also known as Death Domain Containing
 CC Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for
 CC treating, preventing or diagnosing common variable immunodeficiency, X-
 CC linked agammaglobulinemia, severe combined immunodeficiency and Wiskott-
 CC Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,
 CC allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and
 CC asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and
 CC other neurological diseases
 XX
 SQ Sequence 65 AA;
 Query Match 81.8%; Score 338; DB 3; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.7e-35;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRRQOQPAGLGAVYAALERMGLDGC 68
 DB 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRRQOQPAGLGAVYAALERMGLDGC 60
 QY 69 VEDLR 73
 DB 61 VEDLR 65
 RESULT 6
 ID ABG31493
 XX ABG31493 standard; protein; 78 AA.
 AC ABG31493;
 XX
 XX 21-NOV-2002 (first entry)
 XX Human Apo-2bcr associated protein #3.
 XX Human; Apo-2bcr; Apo-2 ligand; programmed cell death; apoptosis;
 KW neurodegenerative disease; autoimmune; inflammatory.
 XX
 OS Homo sapiens.

XX US2002102706-A1.
XX 01-AUG-2002.
XX 21-JUN-2001; 2001US-00887879.
XX 18-JUN-1997; 97US-0049911P.
XX 12-JUN-1998; 98US-00096500.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KF, Chuntharapai A, Gurney A, Kim KJ;
XX Wood WI;
XX WPI; 2002-697823/75.
XX Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in
XX mammalian cells.
XX Disclosure; Page 37; 58pp; English.
XX The present invention relates to the isolation of novel human
XX polypeptides, designated Apo-2Dcr, and the polynucleotide sequences
XX encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is useful
XX for modulating programmed cell death or apoptosis in mammalian cells. Apo
XX -2Dcr can be used to produce apo-2Dcr antibodies which are useful
XX therapeutically, and can cross-react with other receptors for Apo-2
XX ligand to block excessive apoptosis in neurodegenerative diseases, or to
XX block potentially autoimmune or inflammatory effects. Apo-2Dcr antibodies
XX are also useful in immunohistochemistry staining assays or diagnostic
XX assays for Apo-2Dcr, e.g. detecting its expression in specific cells,
XX tissues or serum, and for the affinity purification of Apo-2Dcr from
XX recombinant cell culture or natural sources. The present sequence
XX represents a protein of unknown function relating to the present
XX invention. Note: The present sequence is given in the Seq listing but is
XX not mentioned elsewhere in the specification
XX Sequence 78 AA;
XX Query Match 37.5%; Score 155; DB 5; Length 78;
XX Best Local Similarity 46.1%; Pred. No. 9e-12;
XX Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLRRAEIEAVEVEIGR-FRDOQYEMLKRWROQQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGCLLEDI 76
RESULT 7
ADA49709
ID ADA49709 standard; protein; 78 AA.
XX ADA49709;
XX 20-NOV-2003 (first entry)
XX Death domain of human TNFR1 (htnFR1) protein.
XX Apo-2 ligand inhibitor; Apo-2Li; Apo-3; apoptosis; affinity;
XX competitive-type receptor; binding assay; cancer cell; human;
XX TNF receptor family; htnFR1; death domain; cytostatic.
XX Homo sapiens.
XX US2002192729-A1.
XX 19-DEC-2002.
XX (GETH) GENENTECH INC.

PF 28-MAR-2002; 2002US-00112793.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX 31-MAR-1997; 97US-00828683.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-657226/62.
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
XX in diagnostic assays.
XX Disclosure; Fig 6; 53pp; English.
XX The present invention relates to the isolation of a biologically active
XX Apo-2 ligand inhibitor (Apo-2Li) or Apo-3, and the polynucleotide
XX sequences encoding them. Apo-2Li and Apo-3, are involved in apoptosis. The
XX Apo-2Li and Apo-3 polypeptides are useful in diagnostic assays. Apo-3 or
XX is useful for generating antibodies, as standards in assays for Apo-3 or
XX Apo-2Li, in affinity purification techniques, and in competitive-type
XX receptor binding assays when labelled with radioiodine, enzymes or
XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
XX inducing apoptosis in cancer cells, and thus have therapeutic utility.
XX The present sequence represents the death domain of a human TNF receptor
XX family protein. This sequence is compared with the death domain of human
XX Apo-3.
XX Sequence 78 AA;
XX Query Match 37.5%; Score 155; DB 6; Length 78;
XX Best Local Similarity 46.1%; Pred. No. 8e-12;
XX Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLRRAEIEAVEVEIGR-FRDOQYEMLKRWROQQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGCLLEDI 76
RESULT 8
ADG98745
ID ADG98745 standard; protein; 78 AA.
XX ADG98745;
XX 11-MAR-2004 (first entry)
XX TNFR1 death domain protein.
XX Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
XX cancer; gene therapy.
XX Unidentified.
XX US2003148455-A1.
XX 07-AUG-2003.
XX 06-NOV-2002; 2002US-00288917.
XX 15-MAY-1997; 97US-0046615P.
XX 09-FEB-1998; 98US-0074119P.
XX 14-MAY-1998; 98US-00079029.
XX 02-NOV-2001; 2001US-00052798.
XX (GETH) GENENTECH INC.

54 GAVYAALERMGLDGCVEDLRSRLQGP 80

```
RESULT 13
AAW00208
ID AAW00208 standard; peptide; 64 AA.
XX AC AAW00208;
XX DT 16-APR-1997 (first entry)
XX DE Human p55 tumour necrosis factor receptor death domain motif.
XX KW Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R;
XX KW Fas ligand receptor; Fas/ABO1; ankyrin 1; p55 TNF-R;
XX KW tumour necrosis factor receptor; MORT1; cell cytotoxicity; HIV;
XX KW human immunodeficiency virus; cancer; neoplasia; disease.
XX OS Homo sapiens.
XX PN WO9625941-A1.
XX PD 29-AUG-1996.
XX PF 15-FEB-1996; 96WO-US002326.
XX PR 22-FEB-1995; 95IL-00112742.
XX PR 13-SEP-1995; 95IL-00115289.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PA (WEIN/) WEINURZEL H.
XX FI Wallach D, Boldin MP, Varfolomeev EE, Pancer Z, Mett I;
XX FI Goncharov TM;
XX DR WPI; 1996-402125/40.
XX PT Modulator of regulatory cellular events mediated by "death domain" contg.
XX PT regulatory proteins - useful for modulating functions mediated in cells
XX PT by proteins contg the death domain.
XX PS Claim 9; Fig 1; 74pp; English.
XX CC AAW00207 shows the death domain of the p55 tumour necrosis factor
XX CC receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor
XX CC (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-1
XX CC (which binds to the intracellular portion of (FAS-R)) are also given (see
XX CC AAW00206-07 and AAW00209-W00210). These DDs are used to identify
XX CC compounds capable of modulating activity of the regulatory proteins (p55,
XX CC NGF, TNF and FAS-R ligand, MORT-1) via interaction with the DDs. Such
XX CC modulators which may be antibodies, antisense sequences or ribozymes
XX CC (which can affect the cellular mRNA sequences encoding the proteins) and
XX CC are useful for modulation of effects of the regulatory proteins within
XX CC the cell. Tumour cells, HIV-infected cells or other diseased cells can be
XX CC treated by targeting the cells with animal viral vectors encoding the
XX CC modulators and a viral surface antigen capable of binding to a specific
XX CC receptor. The DDs are characterised by having groups of common amino acid
XX CC residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can
XX CC be aligned to show homology
XX SQ Sequence 64 AA;
Query Match 28.6%; Score 118; DB 2; Length 64;
Best Local Similarity 42.6%; Pred. No. 3.7e-07;
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;
QY 10 WKFFVRLGLREAEIEAVEVEIGR-FRDOQYEMLRKRWQQPAGLGVAVYALRMG----- 64
DB 1 WKFFVRLGLSDHEDIDRLQLGRCLEAQYSMLATWRRTRPR-----EATLELLGRVLR 56
QY 65 ---LDGCV 69
DB 57 DHDLLGLCL 64
```

```
RESULT 14
ADG42594
ID ADG42594 standard; protein; 75 AA.
XX AC ADG42594;
XX DT 26-FEB-2004 (first entry)
XX DE NOVI domain analysis associated protein seq id 47.
XX KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
XX KW NOVX-associated disorder; cancer; NOVX; domain analysis.
XX OS Unidentified.
XX PN US2003204052-A1.
XX PD 30-OCT-2003.
XX PF 04-OCT-2001; 2001US-00970944.
XX PR 04-OCT-2000; 2000US-0237862P.
XX PA (HERR/) HERRMANN J L.
XX PA (RAST/) RASTELLI L.
XX PA (SHIM/) SHIMKETS R A.
XX PI Herrmann JL, Rastelli L, Shimkets RA;
XX DR WPI; 2003-900673/82.
XX PT New NOVX gene or NOVX-specific antibody, useful for preparing a
XX PT composition for treating or preventing a NOVX-associated disorder, e.g.,
XX PT cancer.
XX PS Disclosure; SEQ ID NO 47; 118pp; English.
XX CC The invention describes a new isolated polypeptide comprising: a
XX CC polypeptide or its mature form comprising a sequence not given in the
XX CC specification; or a variant of (A), where one or more amino acid residues
XX CC in the variant differs in no more than 15% from the amino acid sequence
XX CC of the mature form. The pharmaceutical composition may be administered
XX CC via oral, transdermal, rectal or parenteral route. The polypeptide,
XX CC nucleic acid or antibody is useful for preparing a composition for
XX CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
XX CC the amino acid sequence of a protein associated with analysis of domains
XX CC in human NOVI protein.
XX SQ Sequence 75 AA;
Query Match 25.4%; Score 105; DB 7; Length 75;
Best Local Similarity 35.3%; Pred. No. 2.1e-05;
Matches 24; Conservative 12; Mismatches 30; Indels 2; Gaps 1;
QY 1 VMDAVPARRWKBFVRLTGLREAEIEAVEVEIGRFRDOQYEMLRKRWQQ--QPAGLGVAVYA 58
DB 6 LLDDPLGRWRRLARKLGISEEIDQIEHENPRLASPTYQLLDIWEQRGGKNAFVGTLL 65
QY 59 ALERMGLD 66
DB 66 ALRMGRD 73
RESULT 15
AD040451
ID AD040451 standard; protein; 76 AA.
XX AC AD040451;
XX DT 15-JUL-2004 (first entry)
XX DE Human Apo-2 protein #2.
```

XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
KW gene therapy; human.
XX Homo sapiens.
OS
XX US2004009552-A1.
FN
XX 15-JAN-2004.
PD
XX 25-APR-2003; 2003US-00423448.
PF
XX 15-MAY-1997; 97US-0046615P.
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
PR 06-NOV-2002; 2002US-00288917.
XX
XX (GETH) GENENTECH INC.
XX
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI
XX WPI; 2004-090468/09.
DR
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
XX diagnosing, preventing or treating cancer, and in tissue typing or in
PT generating antibodies or transgenic animals.
PT
XX Example 1; SEQ ID NO 14; 53pp; English.
PS
XX The present invention provides novel Apo-2 polypeptide and the encoding
CC polynucleotide capable of modulating apoptosis. The invention is useful
CC in diagnosing, treating and preventing cancer, tissue typing, in
CC generating antibodies and transgenic animals. The invention is also
CC useful in gene therapy. The present sequence is human Apo-2 protein. This
CC sequence is used in the exemplification of the invention
XX
XX Sequence 76 AA;
SQ
Query Match 22.8%; Score 94; DB 8; Length 76;
Best Local Similarity 34.4%; Pred. No. 0.00056;
Matches 22; Conservative 11; Mismatches 29; Indels 2; Gaps 1;
QY 3 DAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRW--RQOQPAGLGAVYAAL 60
Db 3 DLVFPDSHEPLMKLGLMDNEIKVAKAEAGHRDLYTMTLIKVNKTKGRDASVHTLLDAL 62
QY 61 ERMG 64
Db 63 ETIG 66
Search completed: March 20, 2006, 08:04:07
Job time : 81 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:04:14 ; Search time 44 Seconds
(without alignments)
759.690 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDVAPARWKEFVTLGLR.....ERMGLDGCVEDLRLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 736366

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 381 | 92.3 | 74 | 3 | US-09-887-879-15 |
| 2 | 381 | 92.3 | 74 | 3 | US-09-992-964-15 |
| 3 | 381 | 92.3 | 74 | 4 | US-10-207-295-9 |
| 4 | 381 | 92.3 | 74 | 4 | US-10-242-383-15 |
| 5 | 338 | 81.8 | 65 | 3 | US-09-756-854-24 |
| 6 | 338 | 81.8 | 65 | 4 | US-10-041-574-24 |
| 7 | 338 | 81.8 | 65 | 4 | US-10-834-966-24 |
| 8 | 338 | 81.8 | 65 | 6 | US-11-148-333-24 |
| 9 | 155 | 37.5 | 78 | 3 | US-09-887-879-16 |
| 10 | 155 | 37.5 | 78 | 3 | US-09-992-964-16 |
| 11 | 155 | 37.5 | 78 | 4 | US-10-112-793-23 |
| 12 | 155 | 37.5 | 78 | 4 | US-10-207-295-10 |
| 13 | 155 | 37.5 | 78 | 4 | US-10-242-383-16 |
| 14 | 136.5 | 33.1 | 68 | 3 | US-09-756-854-23 |
| 15 | 136.5 | 33.1 | 68 | 4 | US-10-041-574-23 |
| 16 | 136.5 | 33.1 | 68 | 4 | US-10-834-966-23 |
| 17 | 136.5 | 33.1 | 68 | 6 | US-11-148-333-23 |
| 18 | 118 | 28.6 | 64 | 4 | US-10-035-408-3 |
| 19 | 94 | 22.8 | 76 | 4 | US-10-207-295-7 |
| 20 | 83 | 20.1 | 67 | 3 | US-09-756-854-26 |
| 21 | 83 | 20.1 | 67 | 4 | US-10-041-574-26 |
| 22 | 83 | 20.1 | 67 | 4 | US-10-834-966-26 |
| 23 | 83 | 20.1 | 67 | 6 | US-11-148-333-26 |
| 24 | 77.5 | 18.8 | 67 | 6 | US-10-791-513-5 |
| 25 | 74 | 17.9 | 76 | 4 | US-10-207-295-8 |
| 26 | 70.5 | 17.1 | 77 | 4 | US-10-112-793-27 |
| 27 | 70.5 | 17.1 | 77 | 4 | US-10-287-594-7 |

| | | | | | | |
|----|------|------|----|---|----------------------|-------------------|
| 28 | 68 | 16.5 | 67 | 3 | US-09-756-854-25 | Sequence 25, Appl |
| 29 | 68 | 16.5 | 67 | 4 | US-10-041-574-25 | Sequence 25, Appl |
| 30 | 68 | 16.5 | 67 | 4 | US-10-834-966-25 | Sequence 25, Appl |
| 31 | 68 | 16.5 | 67 | 6 | US-11-148-333-25 | Sequence 25, Appl |
| 32 | 64.5 | 15.6 | 65 | 4 | US-10-001-254-56 | Sequence 56, Appl |
| 33 | 64.5 | 15.6 | 65 | 6 | US-11-090-425-56 | Sequence 56, Appl |
| 34 | 63 | 15.3 | 62 | 4 | US-10-424-599-188281 | Sequence 188281, |
| 35 | 60 | 14.5 | 77 | 5 | US-10-656-250-118 | Sequence 118, App |
| 36 | 57.5 | 13.9 | 63 | 4 | US-09-756-854-22 | Sequence 22, Appl |
| 37 | 57.5 | 13.9 | 68 | 3 | US-09-756-854-22 | Sequence 22, Appl |
| 38 | 57.5 | 13.9 | 68 | 3 | US-09-796-692-721 | Sequence 721, App |
| 39 | 57.5 | 13.9 | 68 | 4 | US-10-041-574-22 | Sequence 22, Appl |
| 40 | 57.5 | 13.9 | 68 | 4 | US-10-040-862-721 | Sequence 721, App |
| 41 | 57.5 | 13.9 | 68 | 4 | US-10-057-475B-721 | Sequence 721, App |
| 42 | 57.5 | 13.9 | 68 | 4 | US-10-154-884B-721 | Sequence 721, App |
| 43 | 57.5 | 13.9 | 68 | 4 | US-10-764-324-721 | Sequence 721, App |
| 44 | 57.5 | 13.9 | 68 | 4 | US-10-834-966-22 | Sequence 22, Appl |
| 45 | 57.5 | 13.9 | 68 | 6 | US-11-148-333-22 | Sequence 22, Appl |

ALIGNMENTS

RESULT 1

US-09-887-879-15
; Sequence 15, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-15

Query Match 92.3%; Score 381; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMDVAPARWKEFVTLGLRREAEIEAVEVEIGRFRDQOYEMLRWQOQOQAGLVAAAL 60
Db 1 VMDVAPARWKEFVTLGLRREAEIEAVEVEIGRFRDQOYEMLRWQOQOQAGLVAAAL 60
QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 2

US-09-992-964-15
; Sequence 15, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110

Mon Mar 20 08:26:42 2006

us-10-081-280-6_copy_338_417.rapbm

```

; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-15

Query Match          92.3%; Score 381; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 3
US-10-207-295-9
; Sequence 9, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: APO-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-295-9

Query Match          92.3%; Score 381; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 4
US-10-242-383-15
; Sequence 15, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: APO-2DCR

```

```

; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-15

Query Match          92.3%; Score 381; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 5
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 24;
US-09-756-854-24

Query Match      81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 8
US-11-148-333-24
; Sequence 24, Application US/11148333
; Publication No. US20050239123A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375D1
; CURRENT APPLICATION NUMBER: US/11/148,333
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: human
US-11-148-333-24

Query Match      81.8%; Score 338; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 9
US-09-887-879-16
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 24;
US-09-756-854-24

Query Match      81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAEIEAVEVEIGRFRDQYEMLKRWKRWQOOPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 7
US-10-834-966-24
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
```

US-10-112-793-23
; Sequence 23, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-112-793-23
Query Match 37.5%; Score 155; DB 4; Length 78;
Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGCLLEDI 76
RESULT 12
US-10-207-295-10
; Sequence 10, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: Apo-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216

US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-16
Query Match 37.5%; Score 155; DB 3; Length 78;
Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGCLLEDI 76
RESULT 10
US-09-992-964-16
; Sequence 16, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-16
Query Match 37.5%; Score 155; DB 3; Length 78;
Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGCLLEDI 76
RESULT 11

NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLYING APPLICATION NUMBER: US/09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PF375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-756-854-23

Query Match 33.1%; Score 136.5; DB 3; Length 68;
 Best Local Similarity 46.3%; Pred. No. 8.3e-09;
 Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps

QY 9 RWKEFVRTGLREASIEAVEVEIGR-FRDQQYEMLKRWQR--QQPAGLGAVYAAALRMGL 65
 DB 1 RWKEFVRRLGLSDHEIDRLQLNGRLREAQYSLMATWRRRTTREATLELLGRVLRDMDL 60
 QY 66 DGCVEDL 72
 DB 61 LGLCEDI 67

RESULT 15
 US-10-041-574-23
 ; Sequence 23, Application US/10041574
 ; Publication No. US20020168359A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner L.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; FILE REFERENCE: PF375P1
 ; CURRENT APPLICATION NUMBER: US/10/041,574
 ; CURRENT FILING DATE: 2002-01-10
 ; PRIOR APPLICATION NUMBER: 09/527,236
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/052,991
 ; PRIOR FILING DATE: 1997-06-11
 ; PRIOR APPLICATION NUMBER: 09/095,094
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/126,019
 ; PRIOR FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: 60/134,220
 ; PRIOR FILING DATE: 1999-05-14

```
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-23
```

```
Query Match      33.1%; Score 136.5; DB 4; Length 68;
Best Local Similarity 46.3%; Pred. No. 8.3e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;
```

```
Qy      9 RWKEFVRLGLREAEIEAVEVEIGR-FRDOQYEMLKRWQ--QOPAGLGAVYAALERMGL 65
Db      1 RWKEFVRLGLSDHEIDRLQNGRCLEAQSMLATWRRRTREATLELLGRVLRDMDL 60
```

```
Qy      66 DGCVEDL 72
Db      61 LGCLEDI 67
```

```
Search completed: March 20, 2006, 08:05:09
Job time : 44 secs
```

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

THIS PAGE BLANK (USPTO)

This Page Blank (uspto)

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

THIS PAGE BLANK (USPTO)

A-J-D